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OM protein - protein search, using sw model

Run on: September 9, 2004, 23:42:43 ; Search time 31 Seconds  
(without alignment)  
6.661 Million cell updates/sec

Title: US-10-076-071-1

Perfect score: 23

Sequence: 1 DAHX 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents AA:  
1: /cgn2\_6/prodata/2/iaa/5A.COMB.pep:  
2: /cgn2\_6/prodata/2/iaa/5B.COMB.pep:  
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6: /cgn2\_6/prodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	4	4	US-09-165-926-1
2	23	100.0	4	4	US-09-165-961-1
3	23	100.0	4	4	US-09-165-581-1
4	23	100.0	6	1	US-08-469-856-10
5	23	100.0	8	4	US-09-165-926-2
6	23	100.0	8	4	US-09-165-961-2
7	23	100.0	8	4	US-09-165-581-2
8	23	100.0	11	1	US-08-469-856-9
9	23	100.0	24	2	US-08-702-572-13
10	23	100.0	28	4	US-09-846-329A-1
11	23	100.0	42	4	US-09-480-993-19
12	23	100.0	68	4	US-09-134-000C-4709
13	23	100.0	134	4	US-09-615-192A-316
14	23	100.0	138	4	US-09-134-001C-4838
15	23	100.0	144	4	US-09-328-352-7792
16	23	100.0	168	4	US-09-325-932A-69
17	23	100.0	172	4	US-08-858-207A-499
18	23	100.0	174	2	US-08-683-262B-41
19	23	100.0	174	3	US-09-361-707-41
20	23	100.0	175	4	US-09-134-000C-6037
21	23	100.0	175	4	US-09-328-352-7480
22	23	100.0	175	4	US-09-134-000C-4705
23	23	100.0	183	4	US-09-540-236-3135
24	23	100.0	187	4	US-09-543-681A-4322
25	23	100.0	195	4	US-09-328-352-8131
26	23	100.0	196	4	US-08-679-493A-185
27	23	100.0	200	4	US-09-107-532A-4207

28	23	100.0	201	4	US-09-134-000C-6503	Sequence 6503, Ap
29	23	100.0	207	1	US-07-656-566-2	Sequence 2, Appli
30	23	100.0	211	4	US-09-134-000C-3723	Sequence 3723, Ap
31	23	100.0	211	4	US-09-134-000C-5067	Sequence 5067, Ap
32	23	100.0	213	4	US-09-134-000C-4335	Sequence 4335, Ap
33	23	100.0	214	4	US-09-134-000C-4529	Sequence 4529, Ap
34	23	100.0	218	4	US-09-328-352-4385	Sequence 4385, Ap
35	23	100.0	227	4	US-09-328-352-4162	Sequence 4162, Ap
36	23	100.0	231	1	US-07-656-566-3	Sequence 3, Appli
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38	23	100.0	231	4	US-09-611-216-2	Sequence 2, Appli
39	23	100.0	231	4	US-10-386-972-2	Sequence 29411, A
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42	23	100.0	270	4	US-09-252-991A-16842	Sequence 19255, A
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63	23	100.0	280	4	US-09-553-663-17	Sequence 17, Appl
64	23	100.0	280	4	US-10-062-994-17	Sequence 17, Appl
65	23	100.0	280	4	US-09-811-007A-14	Sequence 14, Appl
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67	23	100.0	286	3	US-09-515-039-78	Sequence 78, Appl
68	23	100.0	288	4	US-09-314-701-32	Sequence 32, Appl
69	23	100.0	295	4	US-09-489-039A-9641	Sequence 9641, Ap
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74	23	100.0	304	4	US-09-543-681A-6103	Sequence 6103, Ap
75	23	100.0	307	4	US-09-543-681A-6403	Sequence 6403, Ap
76	23	100.0	312	4	US-09-107-532A-5684	Sequence 5684, Ap
77	23	100.0	313	4	US-09-540-236-2394	Sequence 2394, Ap
78	23	100.0	337	4	US-09-540-236-3792	Sequence 3792, Ap
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81	23	100.0	355	3	US-09-253-854-5	Sequence 5, Appli
82	23	100.0	355	3	US-08-955-424-5	Sequence 5, Appli
83	23	100.0	373	4	US-09-134-000C-4057	Sequence 4057, Ap
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93	23	100.0	413	4	US-09-134-001C-3361	Sequence 2891, Ap
94	23	100.0	413	4	US-09-134-001C-4058	Sequence 4058, Ap
95	23	100.0	413	4	US-09-134-001C-4975	Sequence 4975, Ap
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97	23	100.0	434	4	US-09-543-681A-7780	Sequence 7780, Ap
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100	23	100.0	448	3	US-09-272-796-2	Sequence 2, Appli

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102	23	100.0	449	2	US-08-869-477-5	Sequence 5, Appli	175	1173	4	US-09-543-681A-7965	Sequence 7965, Ap
103	23	100.0	458	4	US-09-540-236-3313	Sequence 3313, Ap	176	1177	3	US-08-853-160-89	Sequence 8, Appli
104	23	100.0	485	3	US-09-384-212-2	Sequence 2, Appli	177	1184	4	US-10-153-064-99	Sequence 89, Appl
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106	23	100.0	489	4	US-09-134-001C-2920	Sequence 2920, Ap	179	3079	5	PCT-US94-00198-4	Sequence 4, Appli
107	23	100.0	496	4	US-09-312-762A-15	Sequence 15, Appl	180	3696	4	US-09-134-001C-5080	Sequence 5080, Ap
108	23	100.0	508	3	US-09-344-700-4	Sequence 4, Appli	181	20	6	US-08-877-605-193	Sequence 193, App
109	23	100.0	508	4	US-09-563-997A-4	Sequence 639, App	182	20	6	US-08-877-605-194	Sequence 194, App
110	23	100.0	510	4	US-09-198-452A-639	Sequence 3178, Ap	183	20	8	US-09-190-964-13	Sequence 13, Appl
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112	23	100.0	520	1	US-08-706-232-2	Sequence 2, Appli	185	20	34	US-09-205-258-518	Sequence 518, App
113	23	100.0	520	3	US-09-032-365A-15	Sequence 15, Appl	186	20	48	US-08-480-473B-45	Sequence 45, Appl
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115	23	100.0	534	4	US-09-312-762A-4	Sequence 4, Appli	188	20	48	US-09-235-217-45	Sequence 45, Appl
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117	23	100.0	535	4	US-09-312-762A-10	Sequence 10, Appl	190	20	62	US-09-540-236-3270	Sequence 3270, Ap
118	23	100.0	535	4	US-09-312-762A-14	Sequence 14, Appl	191	20	72	US-08-489-039A-12548	Sequence 282, App
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125	23	100.0	609	1	US-08-222-619-3	Sequence 3, Appli	198	20	89	US-07-987-272A-14	Sequence 14, Appl
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128	23	100.0	609	4	US-10-153-064-7	Sequence 7, Appli	201	20	98	US-08-529-055-24	Sequence 24, Appl
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134	23	100.0	621	1	US-08-462-397-2	Sequence 2, Appli	207	20	116	US-09-370-473-10	Sequence 10, Appl
135	23	100.0	651	4	US-10-153-064-133	Sequence 133, App	208	20	116	US-09-010-147B-10	Sequence 10, Appl
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137	23	100.0	652	4	US-10-153-064-99	Sequence 99, Appl	210	20	120	US-09-252-991A-32879	Sequence 32879, A
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141	23	100.0	656	4	US-10-153-064-131	Sequence 131, App	214	20	135	US-08-679-006-29	Sequence 29, Appl
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144	23	100.0	668	4	US-10-153-064-93	Sequence 93, Appl	217	20	144	US-09-441-340-8	Sequence 8, Appli
145	23	100.0	676	4	US-10-153-064-95	Sequence 95, Appl	218	20	144	US-09-441-340-20	Sequence 20, Appl
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147	23	100.0	676	4	US-10-153-064-104	Sequence 104, App	220	20	144	US-09-441-340-26	Sequence 26, Appl
148	23	100.0	676	4	US-10-153-064-127	Sequence 127, App	221	20	144	US-09-441-340-28	Sequence 28, Appl
149	23	100.0	676	4	US-10-153-064-129	Sequence 129, App	222	20	144	US-09-441-340-30	Sequence 30, Appl
150	23	100.0	677	4	US-10-153-064-125	Sequence 125, App	223	20	144	US-09-441-340-32	Sequence 32, Appl
151	23	100.0	680	4	US-10-153-064-123	Sequence 123, App	224	20	146	US-09-252-991A-22791	Sequence 22791, A
152	23	100.0	684	4	US-10-153-064-92	Sequence 92, Appl	225	20	150	US-09-328-352-5004	Sequence 5004, Ap
153	23	100.0	692	4	US-10-153-064-101	Sequence 101, App	226	20	151	US-09-489-039A-13318	Sequence 13318, A
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155	23	100.0	714	4	US-09-828-303-21	Sequence 21, Appl	228	20	158	US-09-252-991A-22916	Sequence 22916, A
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157	23	100.0	741	4	US-09-543-681A-8128	Sequence 8128, Ap	230	20	161	US-09-252-991A-18043	Sequence 18043, A
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160	23	100.0	787	1	US-08-797-689-16	Sequence 16, Appl	233	20	167	US-09-540-236-2159	Sequence 2159, Ap
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262	20	87.0	217	4	US-09-252-991A-19563	Sequence 19563, A	335	20	87.0	287	4	US-10-062-994-19	Sequence 8, Appli
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266	20	87.0	221	1	US-08-222-638B-6	Sequence 6, Appli	339	20	87.0	292	4	US-09-252-991A-17083	Sequence 17083, A
267	20	87.0	221	4	US-09-327-983-13	Sequence 13, Appli	340	20	87.0	297	4	US-09-252-991A-28265	Sequence 28265, A
268	20	87.0	221	4	US-09-327-983-14	Sequence 14, Appli	341	20	87.0	297	4	US-09-395-689-1	Sequence 1, Appli
269	20	87.0	224	4	US-09-082-920-2	Sequence 2, Appli	342	20	87.0	300	4	US-09-563-997A-48	Sequence 48, Appli
270	20	87.0	225	3	US-08-988-251-4	Sequence 4, Appli	343	20	87.0	300	4	US-09-252-991A-31271	Sequence 31271, A
271	20	87.0	225	3	US-09-386-048-4	Sequence 4, Appli	344	20	87.0	303	4	US-09-252-991A-23423	Sequence 23423, A
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273	20	87.0	232	4	US-09-441-340-12	Sequence 12, Appli	346	20	87.0	307	4	US-09-314-701-36	Sequence 36, Appli
274	20	87.0	232	4	US-09-252-991A-27052	Sequence 27052, A	347	20	87.0	308	2	US-08-807-050-1	Sequence 1, Appli
275	20	87.0	232	4	US-09-252-991A-23304	Sequence 23304, A	348	20	87.0	308	2	US-08-807-050-3	Sequence 3, Appli
276	20	87.0	237	4	US-09-252-991A-29337	Sequence 29337, A	349	20	87.0	308	2	US-08-807-050-4	Sequence 4, Appli
277	20	87.0	238	4	US-09-252-991A-29337	Sequence 29337, A	350	20	87.0	311	4	US-09-489-039A-7212	Sequence 7212, Ap
278	20	87.0	239	4	US-09-252-991A-25790	Sequence 25790, A	351	20	87.0	314	4	US-09-690-454-48	Sequence 48, Appli
279	20	87.0	240	4	US-09-252-991A-28112	Sequence 28112, A	352	20	87.0	314	4	US-09-252-991A-19998	Sequence 19998, A
280	20	87.0	241	4	US-09-314-701-62	Sequence 62, Appli	353	20	87.0	315	4	US-09-328-352-6413	Sequence 6413, Ap
281	20	87.0	241	4	US-09-252-991A-18100	Sequence 18100, A	354	20	87.0	317	1	US-08-463-090B-9	Sequence 9, Appli
282	20	87.0	241	4	US-09-252-991A-18244	Sequence 18244, A	355	20	87.0	317	3	US-09-093-522-18	Sequence 18, Appli
283	20	87.0	243	2	US-08-836-620A-8	Sequence 8, Appli	356	20	87.0	317	3	US-09-205-258-504	Sequence 504, App
284	20	87.0	243	2	US-08-836-620A-9	Sequence 9, Appli	357	20	87.0	318	4	US-09-252-991A-22047	Sequence 22047, A
285	20	87.0	243	2	US-08-836-620A-10	Sequence 10, Appli	358	20	87.0	318	4	US-09-543-681A-4414	Sequence 4414, Ap
286	20	87.0	243	4	US-09-489-039A-7807	Sequence 7807, Ap	359	20	87.0	318	4	US-09-252-991A-3676	Sequence 3676, A
287	20	87.0	246	4	US-09-134-001C-3175	Sequence 3175, Ap	360	20	87.0	320	4	US-09-489-039A-8016	Sequence 8016, Ap
288	20	87.0	247	4	US-09-252-991A-22135	Sequence 22135, A	361	20	87.0	320	4	US-09-252-991A-19527	Sequence 19527, A
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290	20	87.0	254	2	US-08-685-992-14	Sequence 14, Appli	363	20	87.0	324	4	US-09-252-991A-18378	Sequence 18378, A
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292	20	87.0	255	4	US-08-976-063B-42	Sequence 446, App	365	20	87.0	325	4	US-09-489-039A-9719	Sequence 9719, Ap
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295	20	87.0	258	5	PCT-US91-05801-29	Sequence 5235, Ap	368	20	87.0	336	4	US-09-252-991A-32686	Sequence 32686, A
296	20	87.0	260	4	US-09-543-681A-5235	Sequence 505, App	369	20	87.0	336	4	US-09-489-039A-7982	Sequence 7982, Ap
297	20	87.0	261	4	US-09-205-258-505	Sequence 1, Appli	370	20	87.0	336	4	US-09-489-039A-7982	Sequence 19234, A
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299	20	87.0	265	4	US-09-252-991A-30000	Sequence 30000, A	372	20	87.0	340	2	US-08-578-592-5	Sequence 5, Appli
300	20	87.0	265	4	US-09-252-991A-30000	Sequence 30000, A	373	20	87.0	340	3	US-09-185-111-5	Sequence 24996, A
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305	20	87.0	275	4	US-09-557-170A-25	Sequence 25, Appli	378	20	87.0	346	4	US-09-489-039A-7673	Sequence 2, Appli
306	20	87.0	277	4	US-09-252-991A-29257	Sequence 23257, A	379	20	87.0	348	4	US-09-931-401B-2	Sequence 2, Appli
307	20	87.0	278	1	US-08-201-697-16	Sequence 16, Appli	380	20	87.0	351	3	US-09-892-188B-2	Sequence 1, Appli
308	20	87.0	278	3	US-08-953-326-16	Sequence 16, Appli	381	20	87.0	351	3	US-09-282-305-4	Sequence 4, Appli
309	20	87.0	278	4	US-09-660-587-2	Sequence 2, Appli	382	20	87.0	351	4	US-09-883-720-4	Sequence 7991, Ap
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395	20	87.0	373	1	US-08-625-209A-2	Sequence 2, Appli	468	20	87.0	483	3	US-09-027-166-9	Sequence 9, Appli
396	20	87.0	374	4	US-09-252-991A-20424	Sequence 20424, A	469	20	87.0	484	4	US-09-252-991A-20787	Sequence 20787, A
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400	20	87.0	378	2	US-08-853-659A-41	Sequence 41, Appl	473	20	87.0	494	3	US-08-988-251-2	Sequence 2, Appli
401	20	87.0	379	2	US-08-553-367A-6	Sequence 6, Appli	474	20	87.0	494	3	US-09-386-048-2	Sequence 2, Appli
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419	20	87.0	406	5	PCT-US91-05801-38	Sequence 38, Appl	492	20	87.0	542	4	US-08-849-180-6	Sequence 6, Appli
420	20	87.0	410	6	5223606-5	Sequence 38, Appl	493	20	87.0	542	4	US-09-356-643B-4	Sequence 4, Appli
421	20	87.0	412	4	US-09-252-991A-18512	Sequence 18512, A	494	20	87.0	549	3	US-09-245-041-9	Sequence 9, Appli
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427	20	87.0	416	4	US-09-657-440-18	Sequence 18, Appl	500	20	87.0	571	4	US-09-134-000C-5368	Sequence 5368, Ap
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430	20	87.0	424	4	US-09-252-991A-32935	Sequence 32935, A	503	20	87.0	574	4	US-09-252-991A-19455	Sequence 19455, A
431	20	87.0	426	3	US-08-737-248-4	Sequence 4, Appli	504	20	87.0	580	4	US-09-252-991A-32531	Sequence 32531, A
432	20	87.0	428	4	US-09-182-625F-9	Sequence 9, Appli	505	20	87.0	580	4	US-09-252-991A-20407	Sequence 20407, A
433	20	87.0	428	4	US-09-252-991A-23934	Sequence 23934, A	506	20	87.0	590	4	US-09-252-991A-22036	Sequence 22036, A
434	20	87.0	428	4	US-09-252-991A-25955	Sequence 25955, A	507	20	87.0	591	2	US-09-252-991A-23447	Sequence 23447, A
435	20	87.0	429	4	US-09-252-991A-27972	Sequence 27972, A	508	20	87.0	593	6	US-08-836-620A-17	Sequence 17, Appl
436	20	87.0	429	4	US-09-252-991A-33116	Sequence 33116, A	509	20	87.0	593	6	5523211-2	Patent No. 5523211
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438	20	87.0	431	4	US-09-252-991A-20267	Sequence 20267, A	511	20	87.0	594	3	US-09-041-886-35	Sequence 35, Appl
439	20	87.0	432	4	US-09-252-991A-30848	Sequence 30848, A	512	20	87.0	595	3	US-08-764-870-12	Sequence 12, Appl
440	20	87.0	436	4	US-09-252-991A-17273	Sequence 17273, A	513	20	87.0	595	3	US-08-980-115-12	Sequence 12, Appl
441	20	87.0	436	4	US-09-252-991A-17926	Sequence 17926, A	514	20	87.0	595	4	US-08-453-998-2	Sequence 2, Appli
442	20	87.0	437	4	US-09-252-991A-31732	Sequence 31732, A	515	20	87.0	595	6	5523211-3	Sequence 21203, A
443	20	87.0	438	4	US-09-252-991A-21521	Sequence 21521, A	516	20	87.0	596	2	US-08-836-620A-16	Sequence 16, Appl
444	20	87.0	440	4	US-09-489-039A-10662	Sequence 10662, A	517	20	87.0	606	2	US-08-883-534-3	Sequence 3, Appli
445	20	87.0	444	4	US-09-252-991A-24777	Sequence 24777, A	518	20	87.0	606	3	US-09-204-764-3	Sequence 3, Appli
446	20	87.0	445	4	US-09-543-681A-4337	Sequence 4337, Ap	519	20	87.0	609	4	US-09-252-991A-24893	Sequence 24893, A
447	20	87.0	446	4	US-09-252-991A-17101	Sequence 17101, A	520	20	87.0	611	3	US-08-904-871-4	Sequence 4, Appli
448	20	87.0	449	4	US-09-134-001C-4409	Sequence 4409, Ap	521	20	87.0	613	3	US-08-622-740-6	Sequence 6, Appli
449	20	87.0	452	3	US-09-052-778-15	Sequence 15, Appl	522	20	87.0	613	3	US-09-122-399-6	Sequence 6, Appli
450	20	87.0	452	4	US-09-252-991A-30368	Sequence 30368, A	523	20	87.0	613	4	US-09-440-689-6	Sequence 6, Appli
451	20	87.0	453	4	US-09-328-352-5069	Sequence 5069, Ap	524	20	87.0	614	3	US-08-447-985-11	Sequence 11, Appl
452	20	87.0	454	4	US-09-252-991A-30164	Sequence 30164, A	525	20	87.0	614	2	US-08-622-740-8	Sequence 8, Appli
453	20	87.0	458	3	US-09-382-305-2	Sequence 2, Appli	526	20	87.0	614	3	US-08-440-689-8	Sequence 8, Appli
454	20	87.0	458	4	US-09-883-720-2	Sequence 2, Appli	527	20	87.0	614	3	US-09-122-399-8	Sequence 8, Appli
455	20	87.0	459	4	US-09-252-991A-20121	Sequence 20121, A	528	20	87.0	614	4	US-08-447-985-13	Sequence 13, Appl
456	20	87.0	465	4	US-09-489-039A-14114	Sequence 14114, A	529	20	87.0	615	3	US-09-042-426-10	Sequence 10, Appl
457	20	87.0	466	4	US-09-252-991A-19221	Sequence 19221, A	530	20	87.0	615	3	US-09-291-238-10	Sequence 10, Appl
458	20	87.0	469	4	US-09-252-991A-28286	Sequence 28286, A	531	20	87.0	615	3	US-09-330-760-10	Sequence 10, Appl
459	20	87.0	470	4	US-09-252-991A-28251	Sequence 28251, A	532	20	87.0	615	3	US-09-328-473-10	Sequence 10, Appl
460	20	87.0	472	4	US-09-489-039A-10123	Sequence 10123, A	533	20	87.0	615	3	US-09-330-737-10	Sequence 10, Appl
461	20	87.0	473	4	US-09-252-991A-24399	Sequence 24399, A	534	20	87.0	615	4	US-09-329-169-10	Sequence 10, Appl
462	20	87.0	476	4	US-09-252-991A-17859	Sequence 17859, A	535	20	87.0	615	4	US-09-330-714A-10	Sequence 10, Appl
463	20	87.0	480	4	US-09-252-991A-26186	Sequence 26186, A	536	20	87.0	615	4	US-09-328-826-10	Sequence 10, Appl
464	20	87.0	481	4	US-09-252-991A-27323	Sequence 27323, A	537	20	87.0	615	4	US-09-289-170-10	Sequence 10, Appl
465	20	87.0	482	4	US-09-252-991A-21327	Sequence 21327, A	538	20	87.0	615	4		

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540	20	87.0	637	4	US-09-489-039A-13362	Sequence 13362, A	613	20	87.0	880	4	US-09-489-039A-12446	Sequence 12446, A
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542	20	87.0	642	4	US-09-252-991A-32104	Sequence 32104, A	615	20	87.0	890	4	US-09-546-013-18	Sequence 18, Appli
543	20	87.0	647	4	US-09-252-991A-25652	Sequence 25652, A	616	20	87.0	890	5	PCT-US94-00545-5	Sequence 5, Appli
544	20	87.0	651	3	US-08-693-940-3	Sequence 3, Appli	617	20	87.0	892	4	PCT-US94-00545-5	Sequence 16, Appli
545	20	87.0	651	4	US-09-566-660-3	Sequence 3, Appli	618	20	87.0	894	2	US-09-585-858-16	Sequence 16, Appli
546	20	87.0	651	4	US-09-252-991A-28603	Sequence 28603, A	619	20	87.0	896	4	US-08-867-941-15	Sequence 15, Appli
547	20	87.0	654	4	US-09-252-991A-18441	Sequence 18441, A	620	20	87.0	898	2	US-08-867-941-15	Sequence 15, Appli
548	20	87.0	654	4	US-09-252-991A-25423	Sequence 25423, A	621	20	87.0	901	4	US-08-867-941-11	Sequence 11, Appli
549	20	87.0	655	1	US-07-736-178C-2	Sequence 2, Appli	622	20	87.0	912	4	US-09-252-991A-25653	Sequence 25653, A
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552	20	87.0	667	4	US-09-252-991A-28436	Sequence 28436, A	625	20	87.0	918	4	US-09-198-452A-1072	Sequence 1072, Ap
553	20	87.0	673	4	US-09-252-991A-29219	Sequence 29219, A	626	20	87.0	921	1	US-09-489-039A-10199	Sequence 10199, A
554	20	87.0	687	4	US-09-252-991A-31650	Sequence 31650, A	627	20	87.0	921	1	US-08-396-479B-2	Sequence 2, Appli
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556	20	87.0	691	4	US-09-252-991A-31413	Sequence 31413, A	629	20	87.0	923	4	US-09-252-991A-22409	Sequence 22409, A
557	20	87.0	692	4	US-09-540-236-2750	Sequence 2750, Ap	630	20	87.0	927	4	US-09-252-991A-4831	Sequence 4831, Ap
558	20	87.0	695	1	US-07-671-817A-5	Sequence 5, Appli	631	20	87.0	931	4	US-09-252-991A-22550	Sequence 22550, A
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564	20	87.0	719	4	US-08-765-907A-15	Sequence 15, Appli	637	20	87.0	976	4	US-08-311-731A-363	Sequence 363, Ap
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569	20	87.0	724	3	US-08-833-391-62	Sequence 62, Appli	642	20	87.0	1049	4	US-09-107-532A-5966	Sequence 5966, Ap
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571	20	87.0	724	5	PCT-US94-10151A-62	Sequence 62, Appli	644	20	87.0	1052	3	US-09-377-310-2	Sequence 2, Appli
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575	20	87.0	734	4	US-09-442-055-2	Sequence 4, Appli	648	20	87.0	1142	3	US-08-904-871-12	Sequence 12, Appli
576	20	87.0	734	4	US-09-442-055-2	Sequence 4, Appli	649	20	87.0	1155	1	US-08-349-867-19	Sequence 19, Appli
577	20	87.0	735	4	US-09-252-991A-17053	Sequence 17053, A	650	20	87.0	1155	1	US-08-349-867-33	Sequence 33, Appli
578	20	87.0	738	4	US-09-252-991A-27291	Sequence 27291, A	651	20	87.0	1155	1	US-08-239-476-19	Sequence 19, Appli
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581	20	87.0	754	4	US-09-489-039A-10222	Sequence 10222, A	654	20	87.0	1155	1	US-08-463-308-2	Sequence 2, Appli
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584	20	87.0	762	4	US-09-252-991A-28078	Sequence 28078, A	657	20	87.0	1155	2	US-08-639-923A-19	Sequence 19, Appli
585	20	87.0	764	4	US-09-252-991A-31816	Sequence 31816, A	658	20	87.0	1155	2	US-08-459-448A-9	Sequence 9, Appli
586	20	87.0	765	2	US-08-663-112-2	Sequence 2, Appli	659	20	87.0	1155	3	US-08-459-595A-9	Sequence 9, Appli
587	20	87.0	773	3	US-08-564-264-1	Sequence 1, Appli	660	20	87.0	1155	3	US-09-021-203-2	Sequence 2, Appli
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592	20	87.0	796	4	US-09-252-991A-17490	Sequence 17490, A	665	20	87.0	1155	4	US-09-547-422-9	Sequence 9, Appli
593	20	87.0	801	4	US-09-252-991A-27870	Sequence 27870, A	666	20	87.0	1155	5	PCT-US95-05431-19	Sequence 19, Appli
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595	20	87.0	809	4	US-09-252-991A-32742	Sequence 32742, A	668	20	87.0	1156	3	US-09-178-252-15	Sequence 15, Appli
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599	20	87.0	833	4	US-09-229-059-4	Sequence 4, Appli	672	20	87.0	1165	5	PCT-US95-05431-33	Sequence 33, Appli
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605	20	87.0	852	4	US-09-585-858-19	Sequence 19, Appli	678	20	87.0	1177	3	US-08-754-490-14	Sequence 14, Appli
606	20	87.0	855	4	US-09-252-991A-26493	Sequence 26493, A	679	20	87.0	1177	3	US-08-754-490-26	Sequence 26, Appli
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609	20	87.0	865	4	US-09-608-821-2	Sequence 2, Appli	682	20	87.0	1177	3	US-08-855-160-6	Sequence 6, Appli
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611	20	87.0	871	3	US-09-245-041-19	Sequence 19, Appli	684	20	87.0	1177	3	US-08-922-505A-12	Sequence 12, Appli

685	20	87.0	1177	3	US-08-922-505A-14	Sequence 14, Appl	758	20	87.0	1181	4	US-09-547-422-11	Sequence 11, Appl
686	20	87.0	1177	3	US-08-922-505A-26	Sequence 26, Appl	759	20	87.0	1181	4	US-09-547-422-13	Sequence 13, Appl
687	20	87.0	1177	3	US-08-922-505A-28	Sequence 28, Appl	760	20	87.0	1181	4	US-09-547-422-15	Sequence 15, Appl
688	20	87.0	1177	3	US-08-922-505A-34	Sequence 34, Appl	761	20	87.0	1181	4	US-09-547-422-17	Sequence 17, Appl
689	20	87.0	1177	3	US-09-260-952A-10	Sequence 10, Appl	762	20	87.0	1181	4	US-09-547-422-28	Sequence 28, Appl
690	20	87.0	1177	3	US-09-260-952A-12	Sequence 12, Appl	763	20	87.0	1181	4	US-09-417-197-133	Sequence 133, Appl
691	20	87.0	1177	3	US-09-260-952A-14	Sequence 14, Appl	764	20	87.0	1182	1	US-08-349-867-34	Sequence 34, Appl
692	20	87.0	1177	3	US-09-260-952A-26	Sequence 26, Appl	765	20	87.0	1182	2	US-08-598-305A-34	Sequence 34, Appl
693	20	87.0	1177	3	US-09-260-952A-28	Sequence 28, Appl	766	20	87.0	1188	1	US-08-233-476-34	Sequence 34, Appl
694	20	87.0	1177	3	US-09-253-341-10	Sequence 10, Appl	767	20	87.0	1188	2	US-08-639-923A-34	Sequence 34, Appl
695	20	87.0	1177	3	US-09-253-341-12	Sequence 12, Appl	768	20	87.0	1188	5	PCT-US95-05431-34	Sequence 34, Appl
696	20	87.0	1177	3	US-09-253-341-14	Sequence 14, Appl	769	20	87.0	1188	1	US-08-602-737-8	Sequence 8, Appl
697	20	87.0	1177	3	US-09-253-341-26	Sequence 26, Appl	770	20	87.0	1193	3	US-08-754-490-30	Sequence 30, Appl
698	20	87.0	1177	3	US-09-253-341-34	Sequence 34, Appl	771	20	87.0	1193	3	US-08-922-505A-30	Sequence 30, Appl
699	20	87.0	1177	3	US-09-253-331A-10	Sequence 10, Appl	772	20	87.0	1193	3	US-09-001-982-8	Sequence 8, Appl
700	20	87.0	1177	3	US-09-253-331A-12	Sequence 12, Appl	773	20	87.0	1193	3	US-09-260-952A-30	Sequence 30, Appl
701	20	87.0	1177	3	US-09-253-331A-14	Sequence 14, Appl	774	20	87.0	1193	3	US-09-253-341-30	Sequence 30, Appl
702	20	87.0	1177	3	US-09-253-331A-26	Sequence 26, Appl	775	20	87.0	1193	3	US-09-253-331A-30	Sequence 30, Appl
703	20	87.0	1177	3	US-09-253-331A-34	Sequence 34, Appl	776	20	87.0	1193	4	US-09-261-040-30	Sequence 30, Appl
704	20	87.0	1177	3	US-09-261-040-10	Sequence 10, Appl	777	20	87.0	1193	4	US-09-916-956A-30	Sequence 30, Appl
705	20	87.0	1177	3	US-09-261-040-12	Sequence 12, Appl	778	20	87.0	1193	4	US-09-873-873-30	Sequence 30, Appl
706	20	87.0	1177	3	US-09-261-040-14	Sequence 14, Appl	779	20	87.0	1193	4	US-09-997-914-30	Sequence 30, Appl
707	20	87.0	1177	3	US-09-261-040-26	Sequence 26, Appl	780	20	87.0	1194	2	US-08-680-326-35	Sequence 35, Appl
708	20	87.0	1177	3	US-09-261-040-28	Sequence 28, Appl	781	20	87.0	1198	3	US-09-794-236-3	Sequence 131, Appl
709	20	87.0	1177	3	US-09-261-040-34	Sequence 34, Appl	782	20	87.0	1217	4	US-09-252-991A-26104	Sequence 26104, A
710	20	87.0	1177	3	US-09-261-040-38	Sequence 38, Appl	783	20	87.0	1235	4	US-08-680-326-36	Sequence 36, Appl
711	20	87.0	1177	3	US-09-916-956A-10	Sequence 10, Appl	784	20	87.0	1235	4	US-09-904-065-6	Sequence 6, Appl
712	20	87.0	1177	3	US-09-916-956A-12	Sequence 12, Appl	785	20	87.0	1235	4	US-09-904-065-8	Sequence 8, Appl
713	20	87.0	1177	3	US-09-916-956A-14	Sequence 14, Appl	786	20	87.0	1235	4	US-09-904-065-10	Sequence 10, Appl
714	20	87.0	1177	3	US-09-916-956A-26	Sequence 26, Appl	787	20	87.0	1235	4	US-09-904-065-16	Sequence 16, Appl
715	20	87.0	1177	3	US-09-916-956A-34	Sequence 34, Appl	788	20	87.0	1235	4	US-09-904-065-17	Sequence 17, Appl
716	20	87.0	1177	3	US-09-916-956A-38	Sequence 38, Appl	789	20	87.0	1235	4	US-09-904-065-18	Sequence 18, Appl
717	20	87.0	1177	3	US-09-873-873-10	Sequence 10, Appl	790	20	87.0	1235	4	US-09-904-065-19	Sequence 19, Appl
718	20	87.0	1177	3	US-09-873-873-12	Sequence 12, Appl	791	20	87.0	1238	4	US-09-252-991A-26363	Sequence 26363, A
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720	20	87.0	1177	3	US-09-873-873-34	Sequence 34, Appl	793	20	87.0	1238	4	US-09-904-065-14	Sequence 14, Appl
721	20	87.0	1177	3	US-09-997-914-10	Sequence 10, Appl	794	20	87.0	1240	4	US-08-680-326-37	Sequence 37, Appl
722	20	87.0	1177	3	US-09-997-914-12	Sequence 12, Appl	795	20	87.0	1240	4	US-09-904-065-4	Sequence 4, Appl
723	20	87.0	1177	3	US-09-997-914-14	Sequence 14, Appl	796	20	87.0	1240	4	US-09-904-065-15	Sequence 15, Appl
724	20	87.0	1177	3	US-09-997-914-26	Sequence 26, Appl	797	20	87.0	1260	3	US-09-245-041-2	Sequence 2, Appl
725	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	798	20	87.0	1318	4	US-09-540-236-3623	Sequence 3623, Ap
726	20	87.0	1177	3	US-09-997-914-38	Sequence 38, Appl	799	20	87.0	1326	4	US-09-252-991A-17932	Sequence 17932, A
727	20	87.0	1177	3	US-09-997-914-44	Sequence 44, Appl	800	20	87.0	1350	4	US-09-245-041-17	Sequence 17, Appl
728	20	87.0	1177	3	US-09-997-914-48	Sequence 48, Appl	801	20	87.0	1395	4	US-09-252-991A-30345	Sequence 30345, A
729	20	87.0	1177	3	US-09-997-914-54	Sequence 54, Appl	802	20	87.0	1427	4	US-09-252-991A-20577	Sequence 20577, A
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732	20	87.0	1177	3	US-09-997-914-70	Sequence 70, Appl	805	20	87.0	1554	4	US-09-182-024A-2	Sequence 2, Appl
733	20	87.0	1177	3	US-09-997-914-76	Sequence 76, Appl	806	20	87.0	1610	4	US-09-568-407-11	Sequence 26814, A
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735	20	87.0	1177	3	US-09-997-914-88	Sequence 88, Appl	808	20	87.0	1788	2	US-08-962-284-2	Sequence 2, Appl
736	20	87.0	1177	3	US-09-997-914-94	Sequence 94, Appl	809	20	87.0	1799	4	US-09-845-583A-6	Sequence 2, Appl
737	20	87.0	1177	3	US-09-997-914-100	Sequence 100, Appl	810	20	87.0	1811	2	US-09-074-658-15	Sequence 15, Appl
738	20	87.0	1177	3	US-09-997-914-106	Sequence 106, Appl	811	20	87.0	2432	3	US-09-074-658-11	Sequence 11, Appl
739	20	87.0	1177	3	US-09-997-914-112	Sequence 112, Appl	812	20	87.0	2439	3	US-09-252-991A-17052	Sequence 17052, A
740	20	87.0	1177	3	US-09-997-914-118	Sequence 118, Appl	813	20	87.0	2639	3	US-09-880-983-3	Sequence 3, Appl
741	20	87.0	1177	3	US-09-997-914-124	Sequence 124, Appl	814	20	87.0	2787	3	US-09-245-041-15	Sequence 15, Appl
742	20	87.0	1177	3	US-09-997-914-130	Sequence 130, Appl	815	20	87.0	3075	2	US-08-460-309-5	Sequence 5, Appl
743	20	87.0	1177	3	US-09-997-914-136	Sequence 136, Appl	816	20	87.0	3075	2	US-08-125-077-5	Sequence 5, Appl
744	20	87.0	1177	3	US-09-997-914-142	Sequence 142, Appl	817	20	87.0	3170	3	US-09-036-987A-4	Sequence 4, Appl
745	20	87.0	1177	3	US-09-997-914-148	Sequence 148, Appl	818	20	87.0	3170	3	US-09-370-700-4	Sequence 4, Appl
746	20	87.0	1177	3	US-09-997-914-154	Sequence 154, Appl	819	20	87.0	3170	3	US-09-603-207-4	Sequence 4, Appl
747	20	87.0	1177	3	US-09-997-914-160	Sequence 160, Appl	820	20	87.0	3816	3	US-09-428-517-3	Sequence 3, Appl
748	20	87.0	1177	3	US-09-997-914-166	Sequence 166, Appl	821	20	87.0	8991	4	US-08-714-741-32	Sequence 32, Appl
749	20	87.0	1177	3	US-09-997-914-172	Sequence 172, Appl	822	20	87.0	8991	4	US-08-041-774-1	Sequence 1, Appl
750	20	87.0	1177	3	US-09-997-914-178	Sequence 178, Appl	823	20	87.0	8991	4	US-08-530-340-7	Sequence 7, Appl
751	20	87.0	1177	3	US-09-997-914-184	Sequence 184, Appl	824	20	87.0	8991	4	US-08-939-002A-8	Sequence 8, Appl
752	20	87.0	1177	3	US-09-997-914-190	Sequence 190, Appl	825	20	87.0	8991	4	US-08-469-141A-9	Sequence 9, Appl
753	20	87.0	1177	3	US-09-997-914-196	Sequence 196, Appl	826	20	87.0	8991	4	US-08-469-141A-26	Sequence 26, Appl
754	20	87.0	1177	3	US-09-997-914-202	Sequence 202, Appl	827	20	87.0	8991	4	PCT-US95-13794-26	Sequence 26, Appl
755	20	87.0	1177	3	US-09-997-914-208	Sequence 208, Appl	828	20	87.0	8991	4		
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## ALIGNMENTS

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; Patent No. 6461875
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Lau, Edward
; APPLICANT: Winkler, James V.
; TITLE OF INVENTION: Test for Rapid Evaluation of Ischemic States and Kit
; FILE REFERENCE: ISC35269-183796
; CURRENT APPLICATION NUMBER: US/09/165,926
; CURRENT FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-165-926-1

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Db 1 DAHK 4

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; Patent No. 6475743
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Lau, Edward
; TITLE OF INVENTION: MARKER USEFUL FOR DETECTION AND MEASUREMENT OF FREE
; FILE REFERENCE: 4172-15
; CURRENT APPLICATION NUMBER: US/09/165,961
; CURRENT FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 4
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; ORGANISM: Homo sapiens
US-09-165-961-1

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; Patent No. 6492179
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Lau, Edward
; APPLICANT: Winkler, James V.
; TITLE OF INVENTION: Test for Rapid Evaluation of Ischemic States and Kit
; FILE REFERENCE: ISC35269-183797
; CURRENT APPLICATION NUMBER: US/09/165,581
; CURRENT FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4
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; ORGANISM: Homo sapiens
US-09-165-581-1

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Db 1 DAHK 4

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RESULT 4
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; Patent No. 5650307
; GENERAL INFORMATION:
; APPLICANT: Sijmons, Peter C.
; APPLICANT: Hoekema, Andreas
; APPLICANT: Dekker, Bernardus M.M.
; APPLICANT: Schrammeijer, Barbara
; APPLICANT: Verwoerd, Tewis C.
; APPLICANT: VandenElzen, Petrus J.M.
; TITLE OF INVENTION: PRODUCTION OF HETEROLOGOUS PROTEINS IN
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,856
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800

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; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 6192-0025.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)887-1500
; TELEFAX: (202)887-0763
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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US-08-469-856-10

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; Patent No. 6461875
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Lau, Edward
; APPLICANT: Winkler, James V.
; TITLE OF INVENTION: Test for Rapid Evaluation of Ischemic States and Kit
; FILE REFERENCE: ISC35269-183796
; CURRENT APPLICATION NUMBER: US/09/165,926
; CURRENT FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
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; TYPE: PRT
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US-09-165-926-2

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Best Local Similarity 100.0%; Pred. No. 3e+05;
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QY 1 DAHK 4
DB 1 DAHK 4

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; Patent No. 6475743
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Lau, Edward
; TITLE OF INVENTION: MARKER USEFUL FOR DETECTION AND MEASUREMENT OF FREE
; FILE REFERENCE: 4172-15
; CURRENT APPLICATION NUMBER: US/09/165,961
; CURRENT FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 3
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US-09-165-961-2

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Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 DAHK 4

RESULT 7
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; Patent No. 6492179
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Lau, Edward
; APPLICANT: Winkler, James V.
; TITLE OF INVENTION: Test for Rapid Evaluation of Ischemic States and Kit
; FILE REFERENCE: ISC35269-183797
; CURRENT APPLICATION NUMBER: US/09/165,581
; CURRENT FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Homo sapiens
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US-09-165-581-2

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Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4
DB 1 DAHK 4

RESULT 8
US-08-469-856-9
; Sequence 9, Application US/08469856
; Patent No. 5650307
; GENERAL INFORMATION:
; APPLICANT: Sijmons, Peter C.
; APPLICANT: Hoekema, Andreas
; APPLICANT: Dekker, Bernardus M.M.
; APPLICANT: Schrammeijer, Barbara
; APPLICANT: Verwoerd, Tewis C.
; APPLICANT: VandenElzen, Petrus J.M.
; TITLE OF INVENTION: PRODUCTION OF HETEROLOGOUS PROTEINS IN
; TITLE OF INVENTION: PLANTS AND PLANT CELLS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,856
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 6192-0025.01

```

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)887-1500  
TELEFAX: (202)887-0763  
TELEX: 90-4030 MESNFOERSWSH  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-469-856-9

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Best Local Similarity 100.0%; Pred. No. 17;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 DAHK 6

## RESULT 9

US-08-702-572-13  
Sequence 13, Application US/08702572  
Patent No. 5965386

GENERAL INFORMATION:  
APPLICANT: Kerry-Williams, Sean M  
APPLICANT: Gilbert, Sarah C  
TITLE OF INVENTION: Yeast Strains and Modified Albumins  
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Centeon L.L.C.  
STREET: 1020 First Avenue  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-1310

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/702,572  
FILING DATE: 11-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 95/23857  
FILING DATE: 1-MAR-1995  
APPLICATION NUMBER: GB 9404270.2  
FILING DATE: 5-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Naomi Biswas  
REGISTRATION NUMBER: 39,384  
REFERENCE/DOCKET NUMBER: CE0114 US

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610/878/4294  
TELEFAX: 610/878/4221  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-702-572-13

Query Match 100.0%; Score 23; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
|||  
Db 20 DAHK 23

## RESULT 10

US-09-846-329A-1  
Sequence 1, Application US/09846329A  
Patent No. 6620786

GENERAL INFORMATION:  
APPLICANT: Jackowski, George  
TITLE OF INVENTION: Biopolymer Marker Indicative of Disease State Having A Molecular Weight of 2937 Daltons  
TITLE OF INVENTION: of 2937 Daltons  
FILE REFERENCE: 2132.052  
CURRENT APPLICATION NUMBER: US/09/846,329A  
CURRENT FILING DATE: 2001-04-30  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1

LENGTH: 28  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-846-329A-1

Query Match 100.0%; Score 23; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
|||  
Db 2 DAHK 5

## RESULT 11

US-09-480-993-19  
Sequence 19, Application US/09480993  
Patent No. 6383790

GENERAL INFORMATION:  
APPLICANT: Shokat, Kevan M.  
TITLE OF INVENTION: High Affinity Kinase Inhibitors for Target Validation  
TITLE OF INVENTION: and Uses Thereof  
FILE REFERENCE: 51538-5001-US  
CURRENT APPLICATION NUMBER: US/09/480,993  
CURRENT FILING DATE: 2000-01-11  
EARLIER APPLICATION NUMBER: US 60/115,340  
EARLIER FILING DATE: 1999-01-11  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 19

LENGTH: 42  
TYPE: PRT

ORGANISM: Saccharomyces cerevisiae  
FEATURE:  
OTHER INFORMATION: Cdc28, cyclin-dependent kinase  
US-09-480-993-19

Query Match 100.0%; Score 23; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
|||  
Db 15 DAHK 18

## RESULT 12

US-09-134-000C-4709  
Sequence 4709, Application US/09134000C  
Patent No. 6617156

GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4709  
; LENGTH: 68  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-4709

Query Match 100.0%; Score 23; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 1 DAHK 4  
Db 35 DAHK 38

## RESULT 13

US-09-615-192A-316  
; Sequence 316, Application US/09615192A  
; Patent No. 6410718  
; GENERAL INFORMATION:  
; APPLICANT: Bloksberg, Leonard N.  
; APPLICANT: Havukkala, Ilkka  
; TITLE OF INVENTION: Materials and Methods for the  
; TITLE OF INVENTION: Modification of Plant Lignin Content  
; FILE REFERENCE: 11000.1003C4U  
; CURRENT APPLICATION NUMBER: US/09/615,192A  
; CURRENT FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 08/975,316  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: US 08/713,000  
; PRIOR FILING DATE: 1996-09-11  
; PRIOR APPLICATION NUMBER: US 09/169,789  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 405  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 316  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Pinus radiata  
US-09-615-192A-316

Query Match 100.0%; Score 23; DB 4; Length 134;  
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 1 DAHK 4  
Db 15 DAHK 18

## RESULT 14

US-09-134-001C-4838  
; Sequence 4838, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4838  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4838

Query Match 100.0%; Score 23; DB 4; Length 138;  
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 1 DAHK 4  
Db 112 DAHK 115

## RESULT 15

US-09-328-352-7792  
; Sequence 7792, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 7792  
; LENGTH: 144  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-7792

Query Match 100.0%; Score 23; DB 4; Length 144;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 4; Conservative 0;

QY 1 DAHK 4  
Db 125 DAHK 128

Search completed: September 9, 2004, 23:48:51  
Job time : 44 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 9, 2004, 23:34:33 ; Search time 113 Seconds

(without alignments)  
11.169 Million cell updates/sec

Title: US-10-076-071-1

Perfect score: 23

Sequence: 1 DAHK 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : SPTREMBL 25.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriaph.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	17	11	Q9QV57
2	23	100.0	21	11	Q9QVA1
3	23	100.0	47	13	Q91093
4	23	100.0	50	17	Q82228
5	23	100.0	56	16	Q88VE6
6	23	100.0	59	10	Q42106
7	23	100.0	66	13	Q91889
8	23	100.0	73	9	Q852W2
9	23	100.0	81	11	Q9R0N2
10	23	100.0	82	9	Q8W6D6
11	23	100.0	82	12	Q56843
12	23	100.0	83	9	Q852V3
13	23	100.0	84	2	Q9RG01
14	23	100.0	87	16	Q9JUN5
15	23	100.0	88	16	Q7VBB7
16	23	100.0	90	17	Q8PYS4

17	23	100.0	91	11	Q9CW67
18	23	100.0	92	2	Q9ZBL9
19	23	100.0	94	16	Q8PG46
20	23	100.0	94	16	Q8ZCA4
21	23	100.0	95	16	Q8R853
22	23	100.0	95	16	Q8RRT9
23	23	100.0	96	11	Q8RA44
24	23	100.0	99	12	Q9PVV5
25	23	100.0	100	16	Q9CFM0
26	23	100.0	102	16	Q9RFX8
27	23	100.0	104	2	Q9RG04
28	23	100.0	104	2	Q9RFZ8
29	23	100.0	104	16	Q8XYZ2
30	23	100.0	107	2	Q93DW4
31	23	100.0	109	1	Q59658
32	23	100.0	109	17	Q8TIL7
33	23	100.0	110	4	Q9BX06
34	23	100.0	110	5	Q86FH2
35	23	100.0	110	16	Q7V709
36	23	100.0	112	16	Q8U5H1
37	23	100.0	114	2	Q9RG07
38	23	100.0	116	2	Q9RAI9
39	23	100.0	116	2	Q9RPP5
40	23	100.0	116	10	Q7XS09
41	23	100.0	118	5	Q9VTJ8
42	23	100.0	118	17	Q980X5
43	23	100.0	120	5	Q8IJ28
44	23	100.0	120	11	Q9D629
45	23	100.0	121	16	Q88061
46	23	100.0	122	16	Q9RTW6
47	23	100.0	122	16	P71946
48	23	100.0	124	10	Q65828
49	23	100.0	125	16	Q9TRJ0
50	23	100.0	128	10	Q8W1R0
51	23	100.0	128	16	Q7U5Y0
52	23	100.0	131	3	Q9UU66
53	23	100.0	132	5	Q95XK0
54	23	100.0	132	12	Q9DST6
55	23	100.0	136	3	Q60092
56	23	100.0	137	11	Q8R213
57	23	100.0	139	16	Q890L9
58	23	100.0	143	10	Q8GUU1
59	23	100.0	144	8	Q952U2
60	23	100.0	146	16	Q88ZN6
61	23	100.0	148	2	Q9S4L7
62	23	100.0	151	16	Q9CJQ5
63	23	100.0	154	16	Q8DDH2
64	23	100.0	155	16	Q9PGZ2
65	23	100.0	155	16	Q8NPV6
66	23	100.0	156	10	Q948A5
67	23	100.0	156	10	Q7XFK9
68	23	100.0	157	10	Q84X70
69	23	100.0	162	16	Q9ED40
70	23	100.0	165	4	Q8TA18
71	23	100.0	166	2	Q9S4Z3
72	23	100.0	168	2	Q87496
73	23	100.0	168	2	Q84GY4
74	23	100.0	168	2	Q8XGT6
75	23	100.0	169	16	Q8XHQ9
76	23	100.0	171	5	Q9VH17
77	23	100.0	171	11	Q9ERG9
78	23	100.0	172	16	Q87F15
79	23	100.0	173	2	Q9S4Z2
80	23	100.0	173	16	Q7WNR3
81	23	100.0	173	16	Q7WB95
82	23	100.0	173	16	Q7VVG1
83	23	100.0	174	13	Q8AXT6
84	23	100.0	175	2	Q53910
85	23	100.0	175	10	Q40848
86	23	100.0	176	16	Q9L001
87	23	100.0	177	16	Q8NMG3
88	23	100.0	179	16	Q8YBD1
89	23	100.0	179	16	Q8FX12

Q9CW67 mus musculus  
Q9ZBL9 mycobacteri  
Q8PG46 xanthomonas  
Q8ZCA4 versinia pe  
Q8R853 thermoanaer  
Q8RRT9 bradyrhizob  
Q8RA44 phodopus su  
Q9PVV5 xestia c-ni  
Q9CFM0 lactococcus  
Q9RFX8 deinococcus  
Q9RG04 mycoplasma  
Q9RFZ8 mycoplasma  
Q8XYZ2 ralstonia s  
Q93DW4 mycoplasma  
Q59658 methanosarc  
Q8TIL7 methanosarc  
Q9BX06 homo sapien  
Q86FH2 schistosoma  
Q7V709 prochloroco  
Q8U5H1 agrobacteri  
Q9RG07 mycoplasma  
Q9RAI9 mycoplasma  
Q9RPP5 ehrlichia c  
Q9XS09 oryza sativ  
Q9VTJ8 drosophila  
Q980X5 sulfolobus  
Q8IJ28 plasmodium  
Q9D629 mus musculus  
Q88061 streptomyce  
Q9RTW6 deinococcus  
P71946 mycobacteri  
Q65828 lycopersico  
Q9TRJ0 neisseria m  
Q8W1R0 synodon dac  
Q7U5Y0 synecococc  
Q9UU66 schizosacch  
Q95XK0 caenorhabdi  
Q9DST6 ascovirus d  
Q60092 schizosacch  
Q8R213 mus musculus  
Q890L9 clostridium  
Q8GUU1 arabidopsis  
Q952U2 stigmatopor  
Q88ZN6 lactobacill  
Q9S4L7 staphylococ  
Q9CJQ5 pasteurella  
Q8DDH2 vibrio valn  
Q9PGZ2 xyella fas  
Q8NPV6 corynebacte  
Q948A5 oryza sativ  
Q7XFK9 oryza sativ  
Q84X70 chlamydomon  
Q9ED40 rhizobium l  
Q8TA18 homo sapien  
Q9S4Z3 ehrlichia m  
Q87496 versinia en  
Q84GY4 photorhabdu  
Q84GT6 versinia en  
Q8XHQ9 clostridium  
Q9VH17 drosophila  
Q9ERG9 mesocricetu  
Q87F15 xyella fas  
Q9S4Z2 ehrlichia m  
Q7WNR3 bordetella  
Q7WB95 bordetella  
Q7VVG1 bordetella  
Q8AXT6 sparus aura  
Q53910 streptomyce  
Q40848 picea glauc  
Q9L001 streptomyce  
Q8NMG3 corynebacte  
Q8YBD1 brucella me  
Q8FX12 brucella su

90	23	100.0	179	16	Q83LW5	Q83LW5 shigella fl	163	23	100.0	273	16	Q8CTH3	Q8cth3 staphylococ
91	23	100.0	184	16	Q83I08	Q83i08 tropheryma	164	23	100.0	274	16	Q8EAX3	Q8eax3 shewanella
92	23	100.0	184	16	Q83G62	Q83g62 tropheryma	165	23	100.0	275	16	Q8CW09	Q8cw09 escherichia
93	23	100.0	185	16	Q8DEA7	Q8dea7 vibrio vuln	166	23	100.0	276	16	Q7UAI1	Q7uai1 shigella fl
94	23	100.0	185	16	Q8DEB6	Q8deb6 vibrio vuln	167	23	100.0	276	2	Q9F475	Q9f475 ehrlichia c
95	23	100.0	187	16	Q99TA5	Q99tas staphylococ	168	23	100.0	276	2	Q9KUJ1	Q9kuj1 peanut witec
96	23	100.0	187	16	Q8EIX9	Q8eix9 shewanella	169	23	100.0	277	2	Q8GGU1	Q8ggul ehrlichia c
97	23	100.0	188	9	Q9ZX97	Q9zx97 bacterioph	170	23	100.0	277	2	Q8G8W7	Q8ggul ehrlichia c
98	23	100.0	191	10	Q9C9T5	Q9c9t5 arabidopsis	171	23	100.0	279	2	Q8G8Q1	Q8ggul ehrlichia c
99	23	100.0	197	13	Q8JH67	Q8jhe7 bufo bufo (	172	23	100.0	280	2	Q52107	Q52107 ehrlichia c
100	23	100.0	198	16	Q83B67	Q83b67 enterococcc	173	23	100.0	283	16	Q7WJG1	Q7wjg1 bordetella
101	23	100.0	200	13	Q7SXN7	Q7sxn7 brachydanio	174	23	100.0	283	16	Q7WAC0	Q7wac0 bordetella
102	23	100.0	204	16	Q83KX5	Q83kx5 shigella fl	175	23	100.0	283	16	Q7VZC8	Q7vzc8 bordetella
103	23	100.0	206	16	Q8PK43	Q8pk43 xanthomonas	176	23	100.0	284	16	Q7W3C5	Q7w3c5 bordetella
104	23	100.0	209	16	Q9RZ87	Q9rz87 deinococcus	177	23	100.0	285	16	Q8U9L1	Q8u9l1 agrobacteri
105	23	100.0	210	11	Q8BK10	Q8bk10 mus musculu	178	23	100.0	285	17	Q58608	Q58608 pyrococcus
106	23	100.0	211	5	Q21501	Q21501 caenorhabdi	179	23	100.0	286	16	Q9PPY5	Q9ppv5 ureaplasma
107	23	100.0	211	10	Q9SHT7	Q9sht7 arabidopsis	180	23	100.0	286	16	Q7WEP4	Q7wep4 bordetella
108	23	100.0	212	4	Q15188	Q15188 homo sapien	181	23	100.0	287	9	Q8LTQ8	Q8ltq8 lactococcus
109	23	100.0	212	16	Q915B3	Q915b3 pseudomonas	182	23	100.0	287	16	Q7VU32	Q7vu32 bordetella
110	23	100.0	213	15	Q91027	Q91027 human immu	183	23	100.0	288	2	Q9ZGJ2	Q9zgj2 ehrlichia c
111	23	100.0	216	5	Q8T010	Q8t010 drosophila	184	23	100.0	288	5	Q8WPU9	Q8wpv9 suberites d
112	23	100.0	216	13	Q9DET0	Q9det0 dicentrarch	185	23	100.0	288	10	Q9XHZ7	Q9xhz7 arabidopsis
113	23	100.0	216	16	Q8DXP3	Q8dpx3 streptococ	186	23	100.0	289	4	Q9H9M2	Q9h9m2 homo sapien
114	23	100.0	219	17	Q8U4N0	Q8u4n0 pyrococcus	187	23	100.0	289	4	Q8TB37	Q8tb37 homo sapien
115	23	100.0	220	11	Q8CA60	Q8ca60 mus musculu	188	23	100.0	289	12	Q7T658	Q7t658 human rhino
116	23	100.0	220	16	Q8CUB5	Q8cub5 staphylococ	189	23	100.0	289	16	Q8ZHH5	Q8zhhs yersinia pe
117	23	100.0	222	5	Q9NFP4	Q9nf94 leishmania	190	23	100.0	290	5	Q19684	Q19684 caenorhabdi
118	23	100.0	222	16	Q8DVJ4	Q8dvj4 streptococ	191	23	100.0	290	16	Q889R3	Q889r3 pseudomonas
119	23	100.0	224	5	Q9NAD4	Q9nad4 caenorhabdi	192	23	100.0	295	16	Q9CPA0	Q9cpa0 pasteurella
120	23	100.0	225	2	Q8RL80	Q8rl80 mycoplasma	193	23	100.0	298	2	P74836	P74836 sphingomona
121	23	100.0	226	16	Q91OE4	Q91oe4 pseudomonas	194	23	100.0	298	13	Q7ZVA2	Q7zva2 brachydanio
122	23	100.0	229	2	Q93EB3	Q93eb3 rhizobium l	195	23	100.0	299	16	Q97IK1	Q97ik1 clostridium
123	23	100.0	229	16	Q930J3	Q930j3 rhizobium m	196	23	100.0	300	12	Q919R6	Q919r6 white spot
124	23	100.0	229	16	Q8UBV8	Q8ubv8 agrobacteri	197	23	100.0	300	12	Q911C5	Q911c5 white spot
125	23	100.0	230	6	Q8SQ56	Q8sq56 sus scrofa	198	23	100.0	302	12	Q7T9Q2	Q7t9q2 adoxophyes
126	23	100.0	230	9	Q64121	Q64121 bacterioph	199	23	100.0	304	16	Q87Q15	Q87q15 vibrio para
127	23	100.0	231	16	Q34581	Q34581 bacillus su	200	23	100.0	305	16	Q8CZS8	Q8czs8 yersinia pe
128	23	100.0	231	2	Q93M48	Q93m48 bacillus th	201	23	100.0	306	10	Q943K3	Q943k3 oryza sativ
129	23	100.0	231	13	Q8AWF0	Q8awf0 epinephelus	202	23	100.0	307	5	Q9VJ94	Q9vj94 drosophila
130	23	100.0	231	13	Q8AVL1	Q8aval epinephelus	203	23	100.0	312	16	Q98K09	Q98k09 rhizobium l
131	23	100.0	231	13	Q7TIA9	Q7tia9 perca flave	204	23	100.0	312	16	Q88DM6	Q88dm6 pseudomonas
132	23	100.0	232	10	Q9LVV7	Q9lvv7 arabidopsis	205	23	100.0	313	5	Q7YZX5	Q7yzx5 trypanosoma
133	23	100.0	235	16	Q9KTG4	Q9ktg4 vibrio chol	206	23	100.0	313	16	Q8F7M9	Q8f7m9 leptospira
134	23	100.0	235	16	Q8EPA6	Q8epa6 oceanobacil	207	23	100.0	314	2	Q8GIY6	Q8giy6 mycoplasma
135	23	100.0	236	17	Q8UOL7	Q8uol7 pyrococcus	208	23	100.0	315	16	Q7WQ23	Q7wq23 bordetella
136	23	100.0	244	5	Q9V5C8	Q9v5c8 drosophila	209	23	100.0	315	16	Q7WC24	Q7wc24 bordetella
137	23	100.0	245	6	Q95J13	Q95j13 pan troglod	210	23	100.0	315	16	Q7VT62	Q7vt62 bordetella
138	23	100.0	246	16	Q83DC4	Q83dc4 coxiella bu	211	23	100.0	316	16	Q92R16	Q92r16 rhizobium m
139	23	100.0	248	12	Q91ID2	Q91id2 lymantria d	212	23	100.0	316	16	Q8DC41	Q8dc41 vibrio vuln
140	23	100.0	248	12	Q99D27	Q99d27 dendrolimus	213	23	100.0	318	4	Q9H8J8	Q9h8j8 homo sapien
141	23	100.0	248	12	Q80HS4	Q80hs4 dendrolimus	214	23	100.0	318	5	Q9BKJ7	Q9bkj7 plasmodium
142	23	100.0	248	12	Q809H2	Q809h2 dendrolimus	215	23	100.0	318	10	Q7YIH6	Q7yih6 oryza sativ
143	23	100.0	248	12	Q8AYY9	Q8ayy9 dendrolimus	216	23	100.0	319	11	Q9CWD8	Q9cwd8 mus musculu
144	23	100.0	249	5	Q9V843	Q9v843 drosophila	217	23	100.0	319	16	Q8YU01	Q8yu01 anabaena sp
145	23	100.0	249	5	Q81308	Q81308 plasmodium	218	23	100.0	320	10	Q8S008	Q8s008 oryza sativ
146	23	100.0	249	10	Q8S1R2	Q8s1r2 oryza sativ	219	23	100.0	320	16	Q988Q5	Q988q5 rhizobium l
147	23	100.0	254	11	Q9DA73	Q9da73 mus musculu	220	23	100.0	322	5	Q23796	Q23796 chironomus
148	23	100.0	254	16	Q98KE3	Q98kp3 rhizobium l	221	23	100.0	323	10	Q8L4X3	Q8l4x3 hordium vul
149	23	100.0	255	2	Q930Z7	Q93uz7 burkholderi	222	23	100.0	324	16	Q8YAX5	Q8yax5 bruceella me
150	23	100.0	256	16	Q8XHG5	Q8xhg5 clostridium	223	23	100.0	325	10	Q94K10	Q94k10 arabidopsis
151	23	100.0	256	16	Q8X7Z4	Q8x7z4 escherichia	224	23	100.0	326	10	Q9SMG8	Q9smg8 oryza sativ
152	23	100.0	256	16	Q7UDM1	Q7udm1 shigella fl	225	23	100.0	326	10	Q8S7Y2	Q8s7y2 oryza sativ
153	23	100.0	257	16	Q899D8	Q899d8 clostridium	226	23	100.0	326	10	P93675	P93675 oryza sativ
154	23	100.0	258	16	Q8A6J3	Q8a6j3 bacteroides	227	23	100.0	326	10	Q7XHB1	Q7xhb1 oryza sativ
155	23	100.0	259	16	Q83M92	Q83m92 shigella fl	228	23	100.0	328	10	Q8LFR5	Q8lfr5 arabidopsis
156	23	100.0	260	13	Q9W6T2	Q9w6t2 cyprinus ca	229	23	100.0	329	5	Q9VFT0	Q9vft0 drosophila
157	23	100.0	262	16	Q914H1	Q914h1 pseudomonas	230	23	100.0	329	5	Q9Y205	Q9y205 ephydatia f
158	23	100.0	264	12	Q86970	Q86970 equine herp	231	23	100.0	329	10	O04326	O04326 arabidopsis
159	23	100.0	268	2	Q54115	Q54115 saccharopol	232	23	100.0	329	10	O8VYL9	O8vyl9 arabidopsis
160	23	100.0	271	2	Q9KI42	Q9ki42 enterococcc	233	23	100.0	330	10	Q9ZRX2	Q9zrx2 triticum ae
161	23	100.0	271	10	Q8S002	Q8s002 oryza sativ	234	23	100.0	330	16	Q97QN8	Q97qn8 streptococ
162	23	100.0	271	16	Q8X284	Q8x284 escherichia	235	23	100.0	330	16	Q8DPQ8	Q8dpq8 streptococ

236 Q89MF0 330 16 Q89MF0 23 100.0  
 237 Q87941 331 2 Q87941 23 100.0  
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Q28907 archaeoglob  
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 Q9A486 caulobacter  
 Q86Z18 neurospora  
 Q47743 enterococcu  
 Q83U28 enterococcu  
 Q81UK7 homo sapien  
 Q81JP4 plasmodium  
 Q8CIFI mus musculu  
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 Q81125 hepatitis b  
 Q99883 hepatitis b  
 Q9QBE6 hepatitis b  
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 Q9QBF0 hepatitis b  
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 Q8KK01 proteus vul  
 Q8BSE0 mus musculu  
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 Q89GN7 pseudomonas  
 Q96BC4 homo sapien  
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 Q95T19 drosophila  
 Q8PJS4 xanthomonas  
 Q8P8C0 xanthomonas  
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 Q8SDA7 pseudomonas  
 Q89GP9 bradyrhizob  
 Q822D7 chlamydia p  
 Q926P4 chlamydia p  
 Q9K1X2 chlamydia p  
 Q9D7P9 mus musculu  
 Q8P762 xanthomonas  
 Q9P712 schizosacch  
 Q9ND6 homo sapien  
 Q7WUH3 clostridium  
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 Q9NCL2 tribolium c  
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 Q81A77 arabidopsis  
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 Q8AVW9 xenopus lae  
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 Q9KEE0 bacillus ha  
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 Q89VY7 bradyrhizob  
 Q9MAU6 arabidopsis  
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 Q8X51 clostridium  
 Q96W14 kluyveromyc  
 Q89J68 pseudomonas  
 Q8XfJ0 salmonella  
 Q95SK9 drosophila  
 Q05461 mycobacteri  
 Q7TVF6 mycobacteri  
 Q86673 streptomyce  
 Q8PS33 methanosarc  
 Q7WXM2 alcaligenes



382	23	100.0	450	16	Q8A246	Q8A246 bacteroides	455	23	100.0	502	16	Q9X8T8	Q9X8T8 streptomyce
383	23	100.0	452	2	Q52018	Q52018 pseudomonas	456	23	100.0	502	16	Q06585	Q06585 mycobacteri
384	23	100.0	452	10	Q7XR14	Q7XR14 oryza sativ	457	23	100.0	502	16	Q7VEU9	Q7VEU9 mycobacteri
385	23	100.0	452	16	Q88EE6	Q88EE6 pseudomonas	458	23	100.0	505	16	Q82RG0	Q82RG0 streptomyce
386	23	100.0	454	13	Q8AWEL	Q8AWEL brachydanio	459	23	100.0	507	2	Q936S5	Q936S5 pseudomonas
387	23	100.0	455	5	Q8IMX2	Q8IMX2 drosophila	460	23	100.0	507	5	Q9VUH7	Q9VUH7 drosophila
388	23	100.0	457	16	Q8UGN7	Q8UGN7 agrobacteri	461	23	100.0	507	11	Q8KOE5	Q8KOE5 mus musculu
389	23	100.0	458	10	Q8AYL9	Q8AYL9 oryza sativ	462	23	100.0	508	5	Q9V3W1	Q9V3W1 drosophila
390	23	100.0	458	10	Q8GRL3	Q8GRL3 oryza sativ	463	23	100.0	508	5	Q8IGL2	Q8IGL2 drosophila
391	23	100.0	458	10	Q7XBZ0	Q7XBZ0 oryza sativ	464	23	100.0	509	16	Q8DOL7	Q8DOL7 yersinia pe
392	23	100.0	458	16	Q9RU65	Q9RU65 deinococcus	465	23	100.0	510	17	Q9Y9C5	Q9Y9C5 aeropyrum p
393	23	100.0	459	16	Q82YE7	Q82YE7 listeria in	466	23	100.0	512	16	Q98N17	Q98N17 rhizobium l
394	23	100.0	459	16	Q8Y3Y5	Q8Y3Y5 listeria mo	467	23	100.0	513	16	Q8E8Q5	Q8E8Q5 shewanella
395	23	100.0	461	10	Q9ZTU6	Q9ZTU6 triticum ae	468	23	100.0	513	17	Q8PZM0	Q8PZM0 methanosarc
396	23	100.0	461	5	Q8IP18	Q8IP18 drosophila	469	23	100.0	518	16	Q91369	Q91369 pseudomonas
397	23	100.0	464	10	Q48933	Q48933 thlaspi goe	470	23	100.0	519	4	Q96HH7	Q96HH7 homo sapien
398	23	100.0	464	17	Q29407	Q29407 archaeoglob	471	23	100.0	519	11	Q8CCL7	Q8CCL7 mus musculu
399	23	100.0	465	8	Q8MA13	Q8MA13 galdieria s	472	23	100.0	520	4	Q8TC50	Q8TC50 homo sapien
400	23	100.0	465	8	Q8LW21	Q8LW21 galdieria s	473	23	100.0	522	9	Q9G0H1	Q9G0H1 roseophage
401	23	100.0	467	10	Q8H846	Q8H846 oryza sativ	474	23	100.0	522	16	Q8VH27	Q8VH27 brucella me
402	23	100.0	467	11	Q8VH50	Q8VH50 mus musculu	475	23	100.0	523	5	Q9VP67	Q9VP67 drosophila
403	23	100.0	467	11	Q8R3D6	Q8R3D6 mus musculu	476	23	100.0	523	5	Q95U04	Q95U04 drosophila
404	23	100.0	467	16	Q8Z621	Q8Z621 salmonella	477	23	100.0	524	10	Q9LMC8	Q9LMC8 arabisopsis
405	23	100.0	467	16	Q8Z7V7	Q8Z7V7 salmonella	478	23	100.0	527	5	Q95QZ7	Q95QZ7 caenorhabdi
406	23	100.0	469	2	Q8RQU8	Q8RQU8 corynebacte	479	23	100.0	527	5	Q01894	Q01894 caenorhabdi
407	23	100.0	469	2	Q9Z466	Q9Z466 corynebacte	480	23	100.0	527	16	Q8YNG9	Q8YNG9 anabaena sp
408	23	100.0	469	5	Q8MMK2	Q8MMK2 dugesia jap	481	23	100.0	529	5	Q962K8	Q962K8 plasmodium
409	23	100.0	469	11	Q8C2R1	Q8C2R1 mus musculu	482	23	100.0	529	5	Q96909	Q96909 plasmodium
410	23	100.0	469	16	Q8NTE1	Q8NTE1 corynebacte	483	23	100.0	529	5	Q95QZ8	Q95QZ8 caenorhabdi
411	23	100.0	470	9	Q9AZ00	Q9AZ00 bacterioph	484	23	100.0	529	5	Q95QZ9	Q95QZ9 caenorhabdi
412	23	100.0	474	16	Q8CQ32	Q8CQ32 staphylococ	485	23	100.0	533	5	Q9NLB8	Q9NLB8 plasmodium
413	23	100.0	475	13	Q8AVV8	Q8AVV8 xenopus lae	486	23	100.0	533	13	Q7ZUE0	Q7ZUE0 brachydanio
414	23	100.0	475	16	Q8FNE6	Q8FNE6 corynebacte	487	23	100.0	533	16	Q8EG41	Q8EG41 shewanella
415	23	100.0	475	17	Q8TW00	Q8TW00 methanopyru	488	23	100.0	534	5	Q8T6T0	Q8T6T0 drosophila
416	23	100.0	479	16	Q8FSK7	Q8FSK7 corynebacte	489	23	100.0	534	5	Q8IGN0	Q8IGN0 drosophila
417	23	100.0	480	16	Q8A0G3	Q8A0G3 bacteroides	490	23	100.0	534	10	Q9SIL5	Q9SIL5 arabisopsis
418	23	100.0	481	3	Q42651	Q42651 schizosacch	491	23	100.0	535	11	Q8R491	Q8R491 rattus norv
419	23	100.0	481	16	Q83H68	Q83H68 tropheryma	492	23	100.0	535	11	Q8K590	Q8K590 mus musculu
420	23	100.0	481	16	Q83FF1	Q83FF1 tropheryma	493	23	100.0	535	16	Q8ERE8	Q8ERE8 oceanobacil
421	23	100.0	482	10	Q9PK89	Q9PK89 arabisopsis	494	23	100.0	536	16	Q7VHQ0	Q7VHQ0 helicobacte
422	23	100.0	482	16	Q83MS0	Q83MS0 tropheryma	495	23	100.0	537	11	Q8R3Z8	Q8R3Z8 rattus norv
423	23	100.0	483	10	Q8S642	Q8S642 oryza sativ	496	23	100.0	537	11	Q8K0B2	Q8K0B2 mus musculu
424	23	100.0	483	16	Q9AEW7	Q9AEW7 caulobacter	497	23	100.0	537	13	Q7ZXE8	Q7ZXE8 xenopus lae
425	23	100.0	484	16	Q9CPK5	Q9CPK5 pasteurella	498	23	100.0	538	5	Q8T3D7	Q8T3D7 caenorhabdi
426	23	100.0	484	16	Q25055	Q25055 helicobacte	499	23	100.0	538	10	Q8H2Q3	Q8H2Q3 oryza sativ
427	23	100.0	484	16	Q9ZMF7	Q9ZMF7 helicobacte	500	23	100.0	538	13	Q7SYA1	Q7SYA1 xenopus lae
428	23	100.0	485	4	Q8U078	Q8U078 homo sapien	501	23	100.0	540	5	Q9UXZ2	Q9UXZ2 caenorhabdi
429	23	100.0	485	6	Q9GLN8	Q9GLN8 pan troglod	502	23	100.0	540	5	Q8T8W3	Q8T8W3 drosophila
430	23	100.0	485	6	Q9GLP7	Q9GLP7 pan troglod	503	23	100.0	541	11	Q8R3Z7	Q8R3Z7 rattus norv
431	23	100.0	485	6	Q9GLP6	Q9GLP6 gorilla gor	504	23	100.0	543	4	Q96CB6	Q96CB6 homo sapien
432	23	100.0	486	6	Q9TSZ0	Q9TSZ0 callithrix	505	23	100.0	543	11	Q8BL28	Q8BL28 mus musculu
433	23	100.0	488	16	Q83CM5	Q83CM5 coxiella bu	506	23	100.0	543	11	Q8BH64	Q8BH64 mus musculu
434	23	100.0	489	11	Q8X3A8	Q8X3A8 mus musculu	507	23	100.0	545	16	Q8ZE13	Q8ZE13 yersinia pe
435	23	100.0	490	12	Q91B79	Q91B79 lasa virus	508	23	100.0	546	4	Q8N514	Q8N514 homo sapien
436	23	100.0	490	12	Q91M18	Q91M18 lasa virus	509	23	100.0	548	11	Q7TPR6	Q7TPR6 mus musculu
437	23	100.0	490	12	Q91MJ0	Q91MJ0 lasa virus	510	23	100.0	548	16	Q9KSV7	Q9KSV7 vibrio chol
438	23	100.0	491	11	Q8K0R1	Q8K0R1 mus musculu	511	23	100.0	548	16	Q87QB3	Q87QB3 vibrio para
439	23	100.0	491	12	Q9DQX8	Q9DQX8 lasa virus	512	23	100.0	549	2	Q84CG8	Q84CG8 actinobacil
440	23	100.0	492	16	Q9K4K3	Q9K4K3 streptomyce	513	23	100.0	549	16	Q97M33	Q97M33 clostridium
441	23	100.0	493	16	Q9JSD2	Q9JSD2 chlamydia p	514	23	100.0	550	11	Q80ZZ0	Q80ZZ0 mus musculu
442	23	100.0	493	16	Q9Z7V6	Q9Z7V6 chlamydia p	515	23	100.0	551	13	Q918S6	Q918S6 oncorhynch
443	23	100.0	494	5	Q9W072	Q9W072 drosophila	516	23	100.0	551	13	Q9PTL6	Q9PTL6 oncorhynch
444	23	100.0	494	16	Q8T460	Q8T460 drosophila	517	23	100.0	551	16	Q89ST6	Q89ST6 bradyrhizob
445	23	100.0	494	16	Q8R9B3	Q8R9B3 thermoaer	518	23	100.0	551	16	Q7VI63	Q7VI63 helicobacte
446	23	100.0	495	5	Q8T3D5	Q8T3D5 caenorhabdi	519	23	100.0	552	16	Q8U6U6	Q8U6U6 agrobacteri
447	23	100.0	496	5	Q94919	Q94919 drosophila	520	23	100.0	553	16	Q8B8Z1	Q8B8Z1 vibrio vuln
448	23	100.0	496	16	Q7UIF5	Q7UIF5 rhodospirell	521	23	100.0	554	10	Q9LU28	Q9LU28 arabisopsis
449	23	100.0	500	2	Q8RN29	Q8RN29 campylobact	522	23	100.0	554	11	Q9JHT9	Q9JHT9 mus musculu
450	23	100.0	500	2	Q8RJJ3	Q8RJJ3 campylobact	523	23	100.0	554	11	Q8C0Q3	Q8C0Q3 mus musculu
451	23	100.0	500	16	Q9PMB6	Q9PMB6 campylobact	524	23	100.0	555	5	Q86S80	Q86S80 caenorhabdi
452	23	100.0	500	17	Q8PUX0	Q8PUX0 methanosarc	525	23	100.0	556	10	Q9AWJ9	Q9AWJ9 oryza sativ
453	23	100.0	501	16	Q8G0T1	Q8G0T1 brucella su	526	23	100.0	556	11	Q8KIX5	Q8KIX5 mus musculu
454	23	100.0	502	2	Q8GPY3	Q8GPY3 pseudomonas	527	23	100.0	561	11	Q8CHI9	Q8CHI9 rattus norv

528	23	100.0	563	16	Q82U87	Q82u87 nitrosomona	601	23	100.0	696	5	Q8T021	Q8t021 drosophila
529	23	100.0	564	10	Q8RXV6	Q8rxv6 arabidopsis	602	23	100.0	699	16	Q8YC56	Q8yc56 bruceella me
530	23	100.0	565	10	Q8S551	Q8s551 cornus seri	603	23	100.0	699	16	Q8FW70	Q8fw70 bruceella su
531	23	100.0	566	11	Q8C9R0	Q8c9r0 mus musculu	604	23	100.0	702	16	Q8XDB2	Q8xdb2 escherichia
532	23	100.0	567	10	Q53377	Q53377 mycobacteri	605	23	100.0	702	16	Q8FJ88	Q8fj88 escherichia
533	23	100.0	570	16	Q7TMD1	Q7twq1 mycobacteri	606	23	100.0	702	16	Q83RX5	Q83rx5 shigella fl
534	23	100.0	571	17	Q97420	Q97420 sulfolobus	607	23	100.0	703	5	Q9NAD6	Q9nad6 caenorhabdi
535	23	100.0	575	17	Q966F0	Q966f0 caenorhabdi	608	23	100.0	703	5	Q9LVA2	Q9lva2 arabidopsis
536	23	100.0	576	5	Q9FGH1	Q9fgf1 arabidopsis	609	23	100.0	706	10	Q8S5J1	Q8s5j1 oryza sativ
537	23	100.0	576	10	Q8SMH4	Q8smh4 encephalito	610	23	100.0	706	16	Q8F5C4	Q8f5c4 leptoeptia
538	23	100.0	579	5	Q8YTY5	Q8yty5 drosophila	611	23	100.0	710	4	Q8NSV2	Q8nsv2 homo sapien
539	23	100.0	583	5	Q7YTY5	Q7yty5 drosophila	612	23	100.0	710	4	Q8CHT1	Q8cht1 mus musculu
540	23	100.0	584	3	Q9P395	Q9p395 neurospora	613	23	100.0	711	11	Q88RL4	Q88rl4 pseudomonas
541	23	100.0	584	3	Q8AE22	Q8ae2 dictyosteli	614	23	100.0	712	3	Q9P7F2	Q9p7f2 schizosacch
542	23	100.0	586	10	Q9F1V6	Q9fiv6 arabidopsis	615	23	100.0	712	3	Q9Y253	Q9y253 homo sapien
543	23	100.0	589	5	Q9NSB9	Q9nsb9 caenorhabdi	616	23	100.0	714	16	Q8PM66	Q8pm66 xanthomonas
544	23	100.0	589	11	Q8OYQ4	Q8oyq4 mus musculu	617	23	100.0	715	10	Q8GUA9	Q8gua9 medicago tr
545	23	100.0	590	13	Q7SXV6	Q7sxy6 brachydanio	618	23	100.0	715	16	Q9PBZ8	Q9pbz8 xyella fas
546	23	100.0	592	5	Q8STB5	Q8stb5 encephalito	619	23	100.0	727	16	P96583	P96583 bacillus su
547	23	100.0	592	11	Q9JLNS	Q9jln5 mus musculu	620	23	100.0	729	10	Q84W64	Q84w64 arabidopsis
548	23	100.0	596	16	Q8VJ30	Q8vj30 mycobacteri	621	23	100.0	730	10	Q49357	Q49357 arabidopsis
549	23	100.0	598	5	Q9W3J9	Q9wj39 drosophila	622	23	100.0	732	2	Q46767	Q46767 escherichia
550	23	100.0	598	16	Q88AU0	Q88aj0 pseudomonas	623	23	100.0	732	5	Q960C3	Q960c3 drosophila
551	23	100.0	599	2	Q9XD73	Q9xd73 streptomyce	624	23	100.0	732	5	Q8RXT2	Q8rxt2 arabidopsis
552	23	100.0	601	16	Q9PMS1	Q9pms1 campylobact	625	23	100.0	732	5	Q8I273	Q8i273 plasmodium
553	23	100.0	603	11	Q9K433	Q9k433 mus musculu	626	23	100.0	734	16	Q8XCX6	Q8xcx6 oceanobacil
554	23	100.0	605	5	Q8SZP3	Q8szp3 drosophila	627	23	100.0	734	16	Q7XR26	Q7xr26 oryza sativ
555	23	100.0	606	16	Q8F8Y9	Q8f8y9 leptospira	628	23	100.0	738	10	Q7XR26	Q7xr26 oryza sativ
556	23	100.0	607	5	Q8T3D6	Q8t3d6 caenorhabdi	629	23	100.0	739	12	Q91WA0	Q91wa0 pothos late
557	23	100.0	608	5	Q9SVB7	Q9svb7 schistosoma	630	23	100.0	740	12	Q84831	Q84831 pothos late
558	23	100.0	610	5	Q9CZJ8	Q9czj8 bombyx mori	631	23	100.0	741	10	Q9LNO1	Q9ln01 arabidopsis
559	23	100.0	613	5	Q8WSPL	Q8wsp1 caenorhabdi	632	23	100.0	742	5	Q9N8X0	Q9n8x0 trypanosoma
560	23	100.0	614	16	Q9ABQ4	Q9abq4 caulobacter	633	23	100.0	747	10	Q9C5F1	Q9c5f1 arabidopsis
561	23	100.0	620	11	Q923H2	Q923h2 mus musculu	634	23	100.0	748	16	Q87D66	Q87d66 xyella fas
562	23	100.0	622	16	Q89Z20	Q89z20 clostridium	635	23	100.0	750	16	Q87LVN0	Q87lvn0 arabidopsis
563	23	100.0	624	16	Q8CJL4	Q8cj14 streptomyce	636	23	100.0	750	16	Q8L328	Q8l328 salmonella
564	23	100.0	625	5	Q8EBQ6	Q8ebq6 drosophila	637	23	100.0	751	16	Q8Z6H1	Q8zeh1 salmonella
565	23	100.0	625	16	Q9CDJ2	Q9cdj2 lactococcus	638	23	100.0	752	4	Q7Z6K8	Q7z6k8 homo sapien
566	23	100.0	628	16	Q7VH11	Q7vnh1 helicobacte	639	23	100.0	752	10	Q43559	Q43559 medicago sa
567	23	100.0	629	16	Q826N5	Q826n5 streptomyce	640	23	100.0	752	16	Q9K109	Q9k109 neisseria m
568	23	100.0	630	4	Q9NVH8	Q9nvh8 homo sapien	641	23	100.0	752	16	Q9JSM8	Q9jsw8 neisseria m
569	23	100.0	631	16	Q8E9Z4	Q8e9z4 shewanella	642	23	100.0	753	10	Q9FGT9	Q9fgt9 arabidopsis
570	23	100.0	635	5	Q9V3G6	Q9v3g6 drosophila	643	23	100.0	753	16	Q8XEL2	Q8xel2 escherichia
571	23	100.0	638	16	Q9W2R9	Q9w2r9 drosophila	644	23	100.0	753	16	Q8FHL1	Q8fhl1 escherichia
572	23	100.0	639	16	Q8XP76	Q8xp76 clostridium	645	23	100.0	753	16	Q7UCI4	Q7uci4 shigella fl
573	23	100.0	641	4	Q60311	Q60311 homo sapien	646	23	100.0	755	16	Q8G7P8	Q8g7p8 bifidobacte
574	23	100.0	642	16	Q8BLH0	Q8blh0 pseudomonas	647	23	100.0	763	10	Q9FZ11	Q9fz11 arabidopsis
575	23	100.0	650	4	Q9NZF0	Q9nzf0 homo sapien	648	23	100.0	764	10	Q7Y208	Q7y208 arabidopsis
576	23	100.0	652	12	Q41929	Q41929 murid herpe	649	23	100.0	765	10	Q42651	Q42651 chenopodium
577	23	100.0	654	5	Q9W359	Q9w359 drosophila	650	23	100.0	766	10	Q43797	Q43797 nicotiana t
578	23	100.0	660	13	Q7ZXT2	Q7zxt2 xenopus lae	651	23	100.0	768	16	Q88LW9	Q88lw9 rhizobium l
579	23	100.0	667	13	Q7ZWX1	Q7zwx1 xenopus lae	652	23	100.0	768	16	P94866	P94866 leuconostoc
580	23	100.0	668	4	Q9H950	Q9h950 homo sapien	653	23	100.0	772	2	Q95TR3	Q95tr3 drosophila
581	23	100.0	668	16	Q9CF31	Q9cf31 lactococcus	654	23	100.0	773	5	Q94CP2	Q94cp2 oryza sativ
582	23	100.0	668	16	Q83RG3	Q83rg3 shigella fl	655	23	100.0	773	10	Q7XAC0	Q7xac0 oryza sativ
583	23	100.0	670	4	Q9HCUG	Q9hcj8 homo sapien	656	23	100.0	773	10	Q89K07	Q89k07 bradyrhizob
584	23	100.0	676	5	Q24085	Q24085 drosophila	657	23	100.0	780	16	Q8YC67	Q8yc67 bruceella me
585	23	100.0	676	5	Q95SQ4	Q95sq4 drosophila	658	23	100.0	783	16	Q8F5C7	Q8f5c7 bruceella su
586	23	100.0	676	5	Q9YQ22	Q9yq22 bactrotera	659	23	100.0	783	16	Q8FW59	Q8fw59 bruceella su
587	23	100.0	677	5	Q9GVN2	Q9gvn2 caenorhabdi	660	23	100.0	784	16	Q8UFU4	Q8ufu4 agrobacteri
588	23	100.0	681	2	Q91US1	Q91us1 rhizobium m	661	23	100.0	785	5	Q86S21	Q86s21 caenorhabdi
589	23	100.0	681	16	Q9SM38	Q9sm38 bradyrhizob	662	23	100.0	785	16	Q7VN79	Q7vn79 haemophilus
590	23	100.0	681	16	Q9SM38	Q9sm38 bradyrhizob	663	23	100.0	786	5	Q9NSB7	Q9nsb7 caenorhabdi
591	23	100.0	685	10	Q9SR82	Q9sr82 arabidopsis	664	23	100.0	786	5	Q9TMD9	Q9tmd9 caenorhabdi
592	23	100.0	685	16	Q98LS4	Q98ls4 rhizobium l	665	23	100.0	787	5	Q9TMD9	Q9tmd9 caenorhabdi
593	23	100.0	686	5	Q8MOP5	Q8mr5 drosophila	666	23	100.0	787	10	Q8S2J2	Q8szj2 arabidopsis
594	23	100.0	686	10	Q9SUF9	Q9suf9 arabidopsis	667	23	100.0	787	10	Q8S1W8	Q8slw8 oryza sativ
595	23	100.0	688	10	Q9JYSK8	Q9jysk8 arabidopsis	668	23	100.0	789	16	Q92QMO	Q92qm0 rhizobium m
596	23	100.0	688	10	Q9JYSK8	Q9jysk8 arabidopsis	669	23	100.0	791	5	Q81SG8	Q81sg8 stylonychia
597	23	100.0	688	16	Q88DI7	Q88di7 pseudomonas	670	23	100.0	791	5	Q86CV7	Q86cv7 stylonychia
598	23	100.0	690	5	Q95XR4	Q95xr4 caenorhabdi	671	23	100.0	791	16	Q9JZB6	Q9jzb6 neisseria m
599	23	100.0	694	11	Q9J3N0	Q9j3n0 mus musculu	672	23	100.0	791	16	Q9JZB6	Q9jzb6 neisseria m
600	23	100.0	696	5	Q9VUZ6	Q9vuz6 drosophila	673	23	100.0	791	16	Q9JUD1	Q9jud1 neisseria m

674	23	100.0	793	5	Q9VXP5	Q9vxp5 drosophila	747	23	100.0	1032	10	Q38766	Q38766 avena sativ
675	23	100.0	793	10	Q9LXK67	Q9lck67 arabidopsis	748	23	100.0	1039	5	Q9GV97	Q9gv97 toxoplasma
676	23	100.0	800	16	Q9CJP2	Q9cjp2 pasteurella	749	23	100.0	1051	11	Q91XT4	Q91xt4 mus musculus
677	23	100.0	802	4	Q9H998	Q9h998 homo sapien	750	23	100.0	1053	16	Q8XRL3	Q8xrl3 ralestonia s
678	23	100.0	803	1	Q87780	Q87780 pyrobaculum	751	23	100.0	1058	11	Q925T1	Q925t1 rattus norv
679	23	100.0	803	17	Q97UH8	Q97uh8 sulfolobus	752	23	100.0	1075	5	Q9NC90	Q9nc90 strongyloce
680	23	100.0	806	16	Q7WXX6	Q7wxk6 bordetella	753	23	100.0	1085	16	Q7U243	Q7u243 mycobacteri
681	23	100.0	807	16	Q8PAG7	Q8pag7 xanthomonas	754	23	100.0	1092	16	Q53720	Q53720 mycobacteri
682	23	100.0	809	10	Q8RQW1	Q8rwi1 arabidopsis	755	23	100.0	1111	10	Q9FZ10	Q9fz10 arabidopsis
683	23	100.0	810	16	Q69650	Q69650 mycobacteri	756	23	100.0	1116	16	Q97KU3	Q97ku3 clostridium
684	23	100.0	810	16	Q7TVY3	Q7tvv3 mycobacteri	757	23	100.0	1123	16	Q89VS9	Q89vs9 bradyrhizob
685	23	100.0	812	16	Q8XPE8	Q8xf8 salmonella	758	23	100.0	1130	11	Q80TZ5	Q80tz5 mus musculus
686	23	100.0	814	16	Q9L749	Q9lt49 arabidopsis	759	23	100.0	1131	5	Q9VLW2	Q9v1w2 drosophila
687	23	100.0	814	11	Q91YT6	Q9lyt6 mus musculus	760	23	100.0	1135	10	Q7XBS9	Q7xbs9 oryza sativ
688	23	100.0	817	16	Q8DCT9	Q8dct9 vibrio vuln	761	23	100.0	1145	10	Q8GHE7	Q8gue7 crymodocosa n
689	23	100.0	822	16	Q8AAE0	Q8aae0 bacteroides	762	23	100.0	1148	10	Q8H977	Q8h977 oryza sativ
690	23	100.0	822	3	Q9P312	Q9p312 neurospora	763	23	100.0	1157	5	Q27088	Q27088 trichomonas
691	23	100.0	826	16	Q7W718	Q7w718 bordetella	764	23	100.0	1157	5	Q27088	Q27088 trichomonas
692	23	100.0	826	16	Q7VTK5	Q7vtx5 bordetella	765	23	100.0	1162	5	Q24818	Q24818 entamoeba h
693	23	100.0	827	16	Q8XDL9	Q8xdl9 escherichia	766	23	100.0	1165	5	Q24860	Q24860 entamoeba h
694	23	100.0	827	16	Q8FAK5	Q8fak5 escherichia	767	23	100.0	1170	16	Q7VBU2	Q7vbu2 prochloroco
695	23	100.0	827	16	Q8D6Y1	Q8d6y1 vibrio vuln	768	23	100.0	1180	5	Q9VPV5	Q9vpv5 drosophila
696	23	100.0	834	10	Q9SVA5	Q9sva5 arabidopsis	769	23	100.0	1191	5	Q9XYX3	Q9xyx3 dictyosteli
697	23	100.0	835	5	Q9NSE8	Q9ns8 caenorhabdi	770	23	100.0	1193	16	Q7V7H1	Q7v7h1 prochloroco
698	23	100.0	837	2	Q93DI1	Q93di1 acinetobact	771	23	100.0	1196	5	Q23866	Q23866 dictyosteli
699	23	100.0	838	5	Q9GDV1	Q9gdv1 drosophila	772	23	100.0	1199	10	Q84R14	Q84r14 arabidopsis
700	23	100.0	844	2	Q93DI2	Q9cvf4 leptospira	773	23	100.0	1215	5	Q9W2K4	Q9w2k4 drosophila
701	23	100.0	844	16	Q82V15	Q82v15 yersinia pe	774	23	100.0	1226	5	Q9V4U3	Q9v4u3 drosophila
702	23	100.0	844	16	Q82V15	Q82v15 yersinia pe	775	23	100.0	1230	10	Q8RU68	Q8ru68 oryza sativ
703	23	100.0	857	16	Q8BDE6	Q8bde6 pseudomonas	776	23	100.0	1235	5	Q8IEN8	Q8ien8 plasmodium
704	23	100.0	865	10	Q9FZB2	Q9fzb2 arabidopsis	777	23	100.0	1249	11	Q80TH4	Q80th4 mus musculus
705	23	100.0	865	16	Q8X957	Q8x957 escherichia	778	23	100.0	1254	13	Q7SYD5	Q7syd5 bradydiano
706	23	100.0	865	16	Q7UDR9	Q7udr9 shigella fl	779	23	100.0	1256	16	Q8DRA6	Q8dra6 streptococ
707	23	100.0	867	10	Q8GZ28	Q8gz28 arabidopsis	780	23	100.0	1257	4	Q43738	Q43738 homo sapien
708	23	100.0	871	16	Q9PZ11	Q9pzi1 campylobact	781	23	100.0	1257	11	Q9Z301	Q9z301 rattus norv
709	23	100.0	872	5	Q8MZH3	Q8mzh3 drosophila	782	23	100.0	1258	5	Q8T6L6	Q8t6l6 drosophila
710	23	100.0	872	5	Q9VGU5	Q9vgu5 drosophila	783	23	100.0	1264	5	Q9V4U4	Q9v4u4 drosophila
711	23	100.0	872	11	Q8KOB3	Q8kob3 mus musculus	784	23	100.0	1267	3	Q8JOT2	Q8jot2 emericeila
712	23	100.0	874	16	Q8DAR2	Q8dar2 vibrio vuln	785	23	100.0	1267	11	Q8OU32	Q8ou32 mus musculus
713	23	100.0	876	2	Q32739	Q32739 clostridium	786	23	100.0	1269	5	Q22855	Q22855 caenorhabdi
714	23	100.0	876	2	Q9KH41	Q9kha1 clostridium	787	23	100.0	1278	5	Q8T6L7	Q8t6l7 drosophila
715	23	100.0	876	16	Q87QX7	Q87qx7 vibrio para	788	23	100.0	1280	16	Q978S7	Q978s7 streptococ
716	23	100.0	877	16	Q87VK1	Q87vk1 pseudomonas	789	23	100.0	1287	5	Q9F930	Q9f930 streptococ
717	23	100.0	879	2	Q06498	Q06498 clostridium	790	23	100.0	1287	5	Q7YVY8	Q7yvy8 drosophila
718	23	100.0	883	9	Q858N4	Q858n4 yersinia pe	791	23	100.0	1302	4	Q9H582	Q9h582 homo sapien
719	23	100.0	884	9	Q9T145	Q9t145 bacterioph	792	23	100.0	1304	5	Q9U3L2	Q9u3l2 caenorhabdi
720	23	100.0	891	5	Q21853	Q21853 caenorhabdi	793	23	100.0	1314	16	Q82BJ3	Q82bj3 streptomyc
721	23	100.0	891	5	Q86B99	Q86b99 drosophila	794	23	100.0	1326	5	Q22240	Q22240 caenorhabdi
722	23	100.0	898	5	Q9WLS3	Q9wls3 drosophila	795	23	100.0	1345	16	Q8Y282	Q8y282 ralestonia s
723	23	100.0	915	5	Q9VDS3	Q9vdk3 drosophila	796	23	100.0	1355	16	Q8XXK6	Q8xxk6 clostridium
724	23	100.0	916	16	Q8FL41	Q8fl41 escherichia	797	23	100.0	1396	5	Q8T3K7	Q8t3k7 drosophila
725	23	100.0	916	16	Q83SM4	Q83sm4 shigella fl	798	23	100.0	1421	10	Q84ZR6	Q84zr6 oryza sativ
726	23	100.0	940	10	Q81502	Q81502 arabidopsis	799	23	100.0	1431	11	Q8K3T7	Q8k3t7 mus musculus
727	23	100.0	942	2	Q938A0	Q938a0 mycobacteri	800	23	100.0	1433	3	Q8TFI7	Q8tfi7 saccharomyc
728	23	100.0	955	4	Q81ZQ4	Q81zq4 homo sapien	801	23	100.0	1445	4	Q9ULL6	Q9ull6 homo sapien
729	23	100.0	955	4	Q7Z4H7	Q7z4h7 homo sapien	802	23	100.0	1462	3	Q42874	Q42874 schizosacch
730	23	100.0	955	5	Q20829	Q20829 caenorhabdi	803	23	100.0	1508	16	Q9A2F8	Q9a2f8 caulobacter
731	23	100.0	960	16	Q8XW6	Q8xw6 ralestonia s	804	23	100.0	1526	5	Q9A538	Q9a538 drosophila
732	23	100.0	963	1	Q977Q8	Q977q8 uncultured	805	23	100.0	1526	5	Q9A538	Q9a538 drosophila
733	23	100.0	967	16	Q8FVJ5	Q8rvj5 brucella su	806	23	100.0	1548	5	Q9V6D5	Q9v6d5 drosophila
734	23	100.0	976	16	Q9AB92	Q9ab92 caulobacter	807	23	100.0	1548	5	Q9NE01	Q9ne01 leishmania
735	23	100.0	979	11	Q9EP71	Q9ep71 mus musculus	808	23	100.0	1556	5	Q9VRP1	Q9vrp1 drosophila
736	23	100.0	982	5	Q81DQ6	Q81dq6 plasmodium	809	23	100.0	1573	5	Q9VMF3	Q9vmf3 drosophila
737	23	100.0	987	11	Q8K166	Q8k166 mus musculus	810	23	100.0	1586	5	Q9SV18	Q9sv18 drosophila
738	23	100.0	992	11	Q7TT14	Q7tt14 mus musculus	811	23	100.0	1590	5	Q18798	Q18798 caenorhabdi
739	23	100.0	992	11	Q8THF6	Q8thf6 mechanosarc	812	23	100.0	1599	9	Q8MX30	Q8mx30 naegleria g
740	23	100.0	999	11	Q8BR49	Q8br49 mus musculus	813	23	100.0	1628	16	Q9EQZ7	Q9eqz7 mycoplasma
741	23	100.0	1007	5	Q9VAE4	Q9vae4 drosophila	814	23	100.0	1750	10	Q9LPC5	Q9lpc5 arabidopsis
742	23	100.0	1026	11	Q9QZYO	Q9qzyo mus musculus	815	23	100.0	1751	5	Q17143	Q17143 drosophila
743	23	100.0	1027	4	Q86VS3	Q86vs3 homo sapien	816	23	100.0	1751	5	Q8ML44	Q8ml44 drosophila
744	23	100.0	1027	4	Q86VS3	Q86vs3 homo sapien	817	23	100.0	1756	10	Q8O975	Q8o975 arabidopsis
745	23	100.0	1028	16	Q9CMNO	Q9cmno pasteurella	818	23	100.0	1773	5	Q17142	Q17142 drosophila
746	23	100.0	1028	16	Q9CMNO	Q9cmno pasteurella	819	23	100.0	1776	5	Q9V6E1	Q9v6e1 drosophila

820	23	100.0	1803	5	Q8MLG1	Q8mlg1 drosophila	893	20	87.0	82	16	Q8UDB5	Q8udb5 agrobacteri
821	23	100.0	1844	5	Q8IE31	Q8ie31 plasmodium	894	20	87.0	83	16	Q8NN4	Q8enn4 rhizobium l
822	23	100.0	1869	5	Q8IC11	Q8ic11 plasmodium	895	20	87.0	84	5	Q45190	Q45190 caenorhabdi
823	23	100.0	1869	5	Q8EN11	Q8en11 caenorhabdi	896	20	87.0	84	16	Q8Y190	Q8y190 brucella me
824	23	100.0	1917	4	Q8H1I9	Q8h1i9 homo sapien	897	20	87.0	84	16	Q8FZM6	Q8fzm6 brucella su
825	23	100.0	1956	4	Q43154	Q43154 homo sapien	898	20	87.0	85	2	Q8RPH8	Q8rph8 desulfitoba
826	23	100.0	1980	12	Q991N2	Q991n2 little cher	899	20	87.0	86	10	Q9FEL4	Q9fel4 nicotiana t
827	23	100.0	2010	5	Q93330	Q93330 caenorhabdi	900	20	87.0	87	10	Q8GVL9	Q8gvl9 nicotiana a
828	23	100.0	2061	5	Q77025	Q77025 drosophila	901	20	87.0	87	16	Q8DLN4	Q8dlm4 synchococc
829	23	100.0	2062	5	Q8ML45	Q8ml45 drosophila	902	20	87.0	87	16	Q8A46	Q8a46 coxiella bu
830	23	100.0	2138	5	Q9XZE3	Q9xze3 amoeba prot	903	20	87.0	88	16	Q87761	Q87761 mycobacteri
831	23	100.0	2141	6	Q8MJ04	Q8mj04 canis famil	904	20	87.0	88	16	Q7ULM0	Q7ulm0 mycobacteri
832	23	100.0	2149	6	Q8MJ03	Q8mj03 saimir bol	905	20	87.0	90	2	Q8RFY9	Q8rfy9 mycoplasma
833	23	100.0	2152	6	Q8MJ06	Q8mj06 papio hamad	906	20	87.0	91	16	Q53401	Q53401 mycobacteri
834	23	100.0	2154	10	Q9ZVC8	Q9zvc8 arabidopsis	907	20	87.0	91	16	Q7U483	Q7u483 synchococc
835	23	100.0	2202	4	Q8N3C0	Q8n3c0 homo sapien	908	20	87.0	91	16	Q7U483	Q7u483 synchococc
836	23	100.0	2205	5	Q8MLG2	Q8mlg2 drosophila	909	20	87.0	92	2	Q8R3V5	Q8r3v5 mycoplasma
837	23	100.0	2205	5	Q8MLG2	Q8mlg2 drosophila	910	20	87.0	93	2	Q41318	Q41318 secale cere
838	23	100.0	2284	5	Q815Y7	Q815y7 plasmodium	911	20	87.0	94	10	Q39966	Q39966 hordeum bog
839	23	100.0	2294	5	Q9VUB7	Q9vub7 drosophila	912	20	87.0	95	10	Q39984	Q39984 hordeum pus
840	23	100.0	2370	5	Q9VEN1	Q9ven1 drosophila	913	20	87.0	95	10	Q39976	Q39976 hordeum lec
841	23	100.0	2383	10	Q8S484	Q8s484 zea mays (m	914	20	87.0	95	10	Q39976	Q39976 hordeum ste
842	23	100.0	2408	5	Q9V549	Q9v549 drosophila	915	20	87.0	95	10	Q39971	Q39971 hordeum chi
843	23	100.0	2430	11	Q55140	Q55140 mus musculu	916	20	87.0	95	16	Q8LX8	Q8lx8 rhizobium l
844	23	100.0	2437	11	Q63725	Q63725 rattus norv	917	20	87.0	95	16	Q7UUX7	Q7uux7 rhodopirell
845	23	100.0	2555	5	Q8T9E3	Q8t9e3 drosophila	918	20	87.0	98	13	Q8QGA7	Q8qga7 oncorhynch
846	23	100.0	2559	5	Q44381	Q44381 drosophila	919	20	87.0	99	16	Q49504	Q49504 mycoplasma
847	23	100.0	2559	5	Q44113	Q44113 drosophila	920	20	87.0	99	16	Q7VUF5	Q7vuf5 helicobacte
848	23	100.0	2559	5	Q9V7X3	Q9v7x3 drosophila	921	20	87.0	101	2	Q86936	Q86936 acinetobact
849	23	100.0	2615	16	Q9CPI1	Q9cp11 pasteurella	922	20	87.0	103	10	Q8LNP7	Q8lnp7 oryza sativ
850	23	100.0	2664	6	Q8WN95	Q8wn95 bos taurus	923	20	87.0	104	10	Q851K8	Q851k8 oryza sativ
851	23	100.0	2747	5	Q8ICL5	Q8icl5 plasmodium	924	20	87.0	104	11	Q8C8L4	Q8c8l4 mus musculu
852	23	100.0	3074	10	Q9SMH5	Q9smh5 chlamydomon	925	20	87.0	104	11	Q8C8L4	Q8c8l4 mus musculu
853	23	100.0	3111	5	Q9VH10	Q9vh10 drosophila	926	20	87.0	104	16	Q92V2	Q92vv2 rhizobium m
854	23	100.0	3225	16	Q9PKM6	Q9pkm6 chlamydia m	927	20	87.0	105	16	Q8XZ46	Q8xz46 ralistonia s
855	23	100.0	3268	3	Q03280	Q03280 saccharomyc	928	20	87.0	106	16	Q8D6R0	Q8d6r0 vibrio vuln
856	23	100.0	3268	5	Q8IC30	Q8ic30 plasmodium	929	20	87.0	108	2	Q8RTC9	Q8rtc9 escherichia
857	23	100.0	3269	12	Q777N5	Q777n5 papaya leaf	930	20	87.0	108	16	Q8EDY0	Q8edy0 shewanella
858	23	100.0	3291	12	Q66225	Q66225 cryphonectr	931	20	87.0	110	11	Q64497	Q64497 mus musculu
859	23	100.0	3542	5	Q9USM2	Q9usm2 plasmodium	932	20	87.0	111	5	Q21111	Q21111 caenorhabdi
860	23	100.0	3674	5	Q9TYG9	Q9tyg9 caenorhabdi	933	20	87.0	112	5	Q8T3C4	Q8t3c4 caenorhabdi
861	23	100.0	3674	5	Q9TW65	Q9tw65 caenorhabdi	934	20	87.0	112	17	Q9YEX4	Q9yex4 aeropyrum p
862	23	100.0	3692	16	Q8CNU9	Q8cnu9 staphylococ	935	20	87.0	114	16	Q8KE96	Q8ke96 chlorobium
863	23	100.0	4024	4	Q8WXX0	Q8wx0 homo sapien	936	20	87.0	114	4	Q96DA6	Q96da6 homo sapien
864	23	100.0	4031	4	Q9Y2F3	Q9y2f3 homo sapien	937	20	87.0	116	11	Q9CQV7	Q9cq7 mus musculu
865	23	100.0	4277	5	Q7YVK3	Q7yv3 trypanosoma	938	20	87.0	116	16	Q837D5	Q837d5 enterococu
866	23	100.0	4861	4	Q15751	Q15751 homo sapien	939	20	87.0	117	3	Q74332	Q74332 schizosacch
867	23	100.0	5106	5	Q9VAV5	Q9vav5 drosophila	940	20	87.0	117	16	Q9ACS9	Q9acs9 streptomyce
868	20	87.0	5106	5	Q8MQB9	Q8mqb9 caenorhabdi	941	20	87.0	117	16	Q82AZ7	Q82az7 streptomyce
869	20	87.0	5106	5	Q8MQB9	Q8mqb9 caenorhabdi	942	20	87.0	118	2	Q936Y7	Q936y7 pseudomonas
870	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	943	20	87.0	118	2	Q936Y7	Q936y7 pseudomonas
871	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	944	20	87.0	121	4	Q8N9K7	Q8nhk1 pseudomonas
872	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	945	20	87.0	122	16	Q9HXL1	Q9hxl1 rhizobium m
873	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	946	20	87.0	122	16	Q9ZUH8	Q9zuh8 rhizobium m
874	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	947	20	87.0	123	16	Q92EV0	Q92ev0 listeria in
875	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	948	20	87.0	123	16	Q92EV0	Q92ev0 listeria in
876	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	949	20	87.0	123	16	Q92EV0	Q92ev0 listeria in
877	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	950	20	87.0	123	16	Q92EV0	Q92ev0 listeria in
878	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	951	20	87.0	124	11	Q9CQ87	Q9cq87 mus musculu
879	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	952	20	87.0	124	11	Q9CQ87	Q9cq87 mus musculu
880	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	953	20	87.0	124	11	Q9CQ87	Q9cq87 mus musculu
881	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	954	20	87.0	124	11	Q9CQ87	Q9cq87 mus musculu
882	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	955	20	87.0	124	11	Q9CQ87	Q9cq87 mus musculu
883	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	956	20	87.0	124	11	Q9CQ87	Q9cq87 mus musculu
884	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	957	20	87.0	124	11	Q9CQ87	Q9cq87 mus musculu
885	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	958	20	87.0	124	11	Q9CQ87	Q9cq87 mus musculu
886	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	959	20	87.0	124	11	Q9CQ87	Q9cq87 mus musculu
887	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	960	20	87.0	124	11	Q9CQ87	Q9cq87 mus musculu
888	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	961	20	87.0	124	11	Q9CQ87	Q9cq87 mus musculu
889	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	962	20	87.0	124	11	Q9CQ87	Q9cq87 mus musculu
890	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	963	20	87.0	124	11	Q9CQ87	Q9cq87 mus musculu
891	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	964	20	87.0	124	11	Q9CQ87	Q9cq87 mus musculu
892	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	965	20	87.0	124	11	Q9CQ87	Q9cq87 mus musculu

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966 20 87.0 136 2 069489 mycobacteri
967 20 87.0 137 4 096AG7
968 20 87.0 137 5 093UJ2
969 20 87.0 137 16 07VNO2
970 20 87.0 138 10 09SMT5
971 20 87.0 138 16 08YMO7
972 20 87.0 138 16 07UB48
973 20 87.0 140 4 09POQ1
974 20 87.0 140 10 08LCT5
975 20 87.0 140 10 084K70
976 20 87.0 140 11 09CZG9
977 20 87.0 140 16 081RG1
978 20 87.0 140 16 081EB4
979 20 87.0 141 16 08XSP6
980 20 87.0 142 16 007579
981 20 87.0 143 10 085OW4
982 20 87.0 144 16 08FAW1
983 20 87.0 145 4 086U32
984 20 87.0 146 16 0831W4
985 20 87.0 147 2 08GNH8
986 20 87.0 147 5 07YB8
987 20 87.0 148 2 09XB81
988 20 87.0 148 9 003943
989 20 87.0 148 16 092X98
990 20 87.0 149 4 08NSB8
991 20 87.0 149 5 07YTE2
992 20 87.0 150 2 054244
993 20 87.0 150 16 098JR4
994 20 87.0 150 16 09X8U9
995 20 87.0 150 16 0833X9
996 20 87.0 151 16 09HXK3
997 20 87.0 151 16 08PK27
998 20 87.0 152 3 096U94
999 20 87.0 152 5 093141
1000 20 87.0 152 16 08F6C3

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## ALIGNMENTS

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RESULT 1
Q9QVS7 PRELIMINARY; PRT; 17 AA.
AC Q9QVS7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Lactate dehydrogenase-A (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95201434; PubMed=7534515;
RA Sandulache R., Preusch W., Chatterjee B., Gimbel W., Graw J.,
RA Favor J.;
RT "Molecular analysis of four lactate dehydrogenase-A mutants in the
RT mouse.";
RL Mamm. Genome 5:777-780(1994).
SQ SEQUENCE 17 AA; 1982 MW; E941E0A3F2477D45 CRC64;

Query Match 100.0%; Score 23; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DAHK 4
DB 9 DAHK 12

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RESULT 2
Q9QVA1

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ID Q9QVA1 PRELIMINARY; PRT; 21 AA.
AC Q9QVA1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 49 kDa protein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=93105636; PubMed=1468220;
RA Zhu L., Crouch R.K.;
RT "Albumin in the cornea is oxidized by hydrogen peroxide.";
RL Cornea 11:567-572(1992).
DR HSP; P02768; IE7H.
DR GO; GO:0005615; C:extracellular space; IEA.
DR GO; GO:0005386; F:carrier activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00277; transport_prot; 1.
SQ SEQUENCE 21 AA; 2429 MW; 26134A3D7CE29FAC CRC64;

Query Match 100.0%; Score 23; DB 11; Length 21;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DAHK 4
DB 1 DAHK 4

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RESULT 3
Q91093 PRELIMINARY; PRT; 47 AA.
AC Q91093;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Prolactin receptor (Fragment).
OS Meleagris gallopavo (Common turkey).
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Ovarian small white follicles;
RA Pitts G.R., You S.K., Foster D.N., El Halawani M.E.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U22946; AAA75040.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER 1
FT NON_TER 47
SQ SEQUENCE 47 AA; 5216 MW; 6PE5C9609B39F509 CRC64;

Query Match 100.0%; Score 23; DB 13; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 DAHK 4
DB 8 DAHK 11

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RESULT 4
Q8ZZ28 PRELIMINARY; PRT; 50 AA.
AC Q8ZZ28;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

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DE Hypothetical protein PAE0471.  
GN PAE0471.  
OS Pyrobaculum aerophilum.  
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;  
OC Thermoproteaceae; Pyrobaculum.  
OX NCBI\_TaxID=13773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;  
RX MEDLINE=21664397; PubMed=11792869;  
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,  
RA Miller J.H.;  
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum  
aerophilum";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).  
DR EMBL; AE009769; AAL62813.1; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 50 AA; 5883 MW; 9351DE9C9A5E1A6E CRC64;  
Query Match 100.0%; Score 23; DB 17; Length 50;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DAHK 4  
Db 15 DAHK 18  
RESULT 5  
ID Q88VE6 PRELIMINARY; PRT; 56 AA.  
AC Q88VE6;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Hypothetical protein.  
GN LP2112.  
OS Lactobacillus plantarum.  
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;  
OC Lactobacillus.  
OX NCBI\_TaxID=1590;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NCIMB 8826 / WCFS1;  
RX MEDLINE=22480296; PubMed=12566566;  
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,  
RA Kuipers O.P., Leer R., Turchini R., Peters S.A., Sandbrink H.M.,  
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,  
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,  
RA De Vos W.M., Siezen R.J.;  
RT "Complete genome sequence of Lactobacillus plantarum WCFS1";  
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 56 AA; 6438 MW; 78C141687E7FF005 CRC64;  
Query Match 100.0%; Score 23; DB 16; Length 56;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DAHK 4  
Db 53 DAHK 56  
RESULT 6  
ID Q42106 PRELIMINARY; PRT; 59 AA.  
AC Q42106;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Protein kinase inhibitor (Fragment).

OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia; TISSUE=Seedling;  
RA Hofte H.;  
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.  
DR EMBL; Z26527; CAA81298.1; -.  
DR HSSP; P29312; 1A38.  
DR GO; GO:0016301; F:kinase activity; IEA.  
DR GO; GO:0019904; F:protein domain specific binding; IEA.  
DR InterPro; IPR000308; 14-3-3.  
DR Pfam; PF00244; 14-3-3; 1.  
DR PRODOM; PD000600; 14-3-3; 1.  
DR PROSITE; PS00797; 1433\_2; 1.  
KW Kinase.  
FT NON TER 1  
SQ SEQUENCE 59 AA; 6320 MW; 080C0F25F5A6C889 CRC64;  
Query Match 100.0%; Score 23; DB 10; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DAHK 4  
Db 41 DAHK 44  
RESULT 7  
ID Q91889 PRELIMINARY; PRT; 66 AA.  
AC Q91889  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Somatolactin precursor (Fragment).  
OS Oncorhynchus tshawytscha (Chinook salmon) (King salmon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
OX NCBI\_TaxID=74940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=VARIOUS STRAINS;  
RA Ford M.J.;  
RT "Effects of natural selection on patterns of DNA sequence variation at  
the transferrin, somatolactin, and p53 genes within and among chinook  
salmon (Oncorhynchus tshawytscha) populations.";  
RL Mol. Ecol. 9:0-0(2000).  
DR EMBL; AF223890; AAF81065.1; -.  
DR EMBL; AF223821; AAF81019.1; -.  
DR EMBL; AF223824; AAF81021.1; -.  
DR EMBL; AF223827; AAF81023.1; -.  
DR EMBL; AF223830; AAF81025.1; -.  
DR EMBL; AF223833; AAF81027.1; -.  
DR EMBL; AF223836; AAF81029.1; -.  
DR EMBL; AF223839; AAF81031.1; -.  
DR EMBL; AF223842; AAF81033.1; -.  
DR EMBL; AF223845; AAF81035.1; -.  
DR EMBL; AF223848; AAF81037.1; -.  
DR EMBL; AF223851; AAF81039.1; -.  
DR EMBL; AF223854; AAF81041.1; -.  
DR EMBL; AF223857; AAF81043.1; -.  
DR EMBL; AF223860; AAF81045.1; -.  
DR EMBL; AF223863; AAF81047.1; -.  
DR EMBL; AF223866; AAF81049.1; -.  
DR EMBL; AF223869; AAF81051.1; -.  
DR EMBL; AF223872; AAF81053.1; -.  
DR EMBL; AF223875; AAF81055.1; -.  
DR EMBL; AF223878; AAF81057.1; -.

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DR EMBL; AF223881; AAF81059.1; -.
DR EMBL; AF223884; AAF81061.1; -.
DR EMBL; AF223887; AAF81063.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
FT NON TER 1
SQ SEQUENCE 66 AA; 7822 MW; 3CD2A6837C2E359A CRC64;

Query Match 100.0%; Score 23; DB 13; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4
DB 42 DAHK 45

RESULT 8
Q852W2 PRELIMINARY; PRT; 73 AA.
AC Q852W2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp243.
GN G243.
OS Mycobacteriophage Bx21.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=205877;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22592660; PubMed=12705866;
RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Panunzio N.R.,
RA Brucker W., Kumar V., Kandaamy J., Keenan L., Bardarov S.,
RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
RA Hatfull G.F.;
RT "Origins of highly mosaic mycobacteriophage genomes.";
RL Cell 113:171-182(2003).
DR EMBL; AV129337; AAN16875.1; -.
SQ SEQUENCE 73 AA; 8001 MW; 0F08C6D4BB6D241B CRC64;

Query Match 100.0%; Score 23; DB 9; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4
DB 53 DAHK 56

RESULT 9
Q9RON2 PRELIMINARY; PRT; 81 AA.
AC Q9RON2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LR11 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20027760; PubMed=10559012;
RA Kanaki T., Bujo H., Hirayama S., Ishii I., Morisaki N.,
RA Schneider W.J., Saito Y.;
RT "Expression of LR11, a mosaic LDL receptor family member, is markedly
increased in atherosclerotic lesions.";
RL Arterioscler. Thromb. Vasc. Biol. 19:2687-2695(1999).
DR EMBL; AB026993; BAA86122.1; -.
DR InterPro; IPR008957; FN_III-like.
FT NON TER 1
FT NON TER 81
SQ SEQUENCE 81 AA; 8769 MW; 5E2C718C72EEE013 CRC64;

Query Match 100.0%; Score 23; DB 11; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4
DB 11 DAHK 14

RESULT 10
Q8W6D6 PRELIMINARY; PRT; 82 AA.
AC Q8W6D6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Prim-VSK.
GN ORF82.
OS Vibrio phage VSK.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=181604;
RN [1]
RP SEQUENCE FROM N.A.
RX Basu N., Kar S., Ghosh R.K.;
RT "Molecular analysis of filamentous phage VSK of Vibrio cholerae 0139:
A possible clue to genetic transmission.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF453500; AAL49735.1; -.
SQ SEQUENCE 82 AA; 8933 MW; 32E495E7C265A0A9 CRC64;

Query Match 100.0%; Score 23; DB 9; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4
DB 52 DAHK 55

RESULT 11
O56843 PRELIMINARY; PRT; 82 AA.
ID O56843;
AC O56843;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Vibrio cholerae O139 fsl phage.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=70203;
RN [1]
RP SEQUENCE FROM N.A.
RA Homma Y.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97457190; PubMed=9311128;
RA Ebara M., Shimodori S., Kojima F., Ichinose Y., Hirayama T.,
RA Albert M.J., Supawat K., Homma Y., Iwanaga M., Amako K.;
RT "Characterization of filamentous phage of Vibrio cholerae O139 and
O1.";
RL FEMS Microbiol. Lett. 154:293-301(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98201718; PubMed=9540841;

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RA Honma Y., Ikema M., Toma C., Ehara M., Iwanaga M.:  
 RT "Molecular analysis of a filamentous phage (fsl) of *Vibrio cholerae*  
 RL O139.",  
 RL Biochim. Biophys. Acta 1362:109-115(1997).  
 DR EMBL: D89074; BAA24170.1; -.  
 KW Hypothetical protein.  
 SQ SEQUENCE 82 AA; 8928 MW; B11D180214634BB3 CRC64;

Query Match 100.0%; Score 23; DB 12; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 Db 52 DAHK 55

## RESULT 12

Q852V3 PRELIMINARY; PRT; 83 AA.  
 AC Q852V3;  
 DT 01-JUN-2003 (TREMELrel. 24, Created)  
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)  
 DE Gp109.  
 GN 109.  
 OS Mycobacteriophage Bx1.  
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.  
 OX NCBI\_TaxID=205877;  
 RN [1]\_TaxID=205877;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22592860; PubMed=12705866;  
 RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,  
 RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Panunzio N.R.,  
 RA Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,  
 RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,  
 RA Hatfull G.F.;  
 RT "Origins of highly mosaic mycobacteriophage genomes.";  
 RL Cell 113:171-182(2003).  
 DR EMBL: AY129337; AAN16884.1; -.  
 SQ SEQUENCE 83 AA; 9426 MW; 32B2E3A17FBA92F8 CRC64;

Query Match 100.0%; Score 23; DB 9; Length 83;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 Db 42 DAHK 45

## RESULT 13

Q9RG01 PRELIMINARY; PRT; 84 AA.  
 AC Q9RG01;  
 DT 01-MAY-2000 (TREMELrel. 13, Created)  
 DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Fructose biphosphate aldolase (EC 4.1.2.13) (Fragment).  
 GN FBA.  
 OS Mycoplasma capricolum subsp. capricolum.  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
 OX NCBI\_TaxID=40479;  
 RN [1]\_TaxID=40479;  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=7986;  
 RX MEDLINE=20193983; PubMed=10727835;  
 RA Thiaucourt F., Lorenzon S., David A., Beard A.;  
 RT "Phylogeny of the Mycoplasma mycoides cluster as shown by sequencing  
 RT of a putative membrane protein gene.";  
 RL Vet. Microbiol. 72:251-268(2000).  
 DR EMBL: AF162994; AAF15246.1; -.  
 GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.

DR GO: 0016829; F:lyase activity; IEA.  
 DR GO: 0008270; F:zinc ion binding; IEA.  
 DR GO: 0006096; P:glycolysis; IEA.  
 DR InterPro: IPR000771; K\_bp\_aldolase.  
 DR Pfam: PF01116; F\_bp\_aldolase; 1.  
 DR ProDom: PD002376; K\_bp\_aldolase; 1.  
 KW Lyase.  
 FT NON TER 84 84  
 SQ SEQUENCE 84 AA; 9422 MW; C8B61DB0474EB906 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 Db 43 DAHK 46

## RESULT 14

Q9JUN5 PRELIMINARY; PRT; 87 AA.  
 AC Q9JUN5;  
 DT 01-OCT-2000 (TREMELrel. 15, Created)  
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)  
 DE Hypothetical protein NMA1220.  
 GN NMA1220.  
 OS Neisseria meningitidis (serogroup A).  
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;  
 OX Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=65699;  
 RN [1]\_TaxID=65699;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Z2491 / Serogroup A / Serotype 4A;  
 RX MEDLINE=20222556; PubMed=10761919;  
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,  
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,  
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,  
 RA Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,  
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,  
 RA Whitehead S., Spratt B.G., Barrall B.G.;  
 RT "Complete DNA sequence of a serogroup A strain of *Neisseria*  
 RT meningitidis Z2491.";  
 RL Nature 404:502-506(2000).  
 DR EMBL: AL162755; CAB84480.1; -.  
 DR PIR: C81890; C81890.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 87 AA; 9635 MW; 80058F6D4C9ADEA2 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 87;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 Db 46 DAHK 49

## RESULT 15

Q7VBB7 PRELIMINARY; PRT; 88 AA.  
 AC Q7VBB7;  
 DT 01-OCT-2003 (TREMELrel. 25, Created)  
 DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
 DE Putative heme iron utilization protein.  
 GN HUGZ OR PRO1180.  
 OS *Prochlorococcus marinus*.  
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;  
 OC *Prochlorococcus*.  
 OX NCBI\_TaxID=1219;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=SARG / CCMP 1375 / SS120;  
 RX MEDLINE=22810154; PubMed=12917486;  
 RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,  
 RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,  
 RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,  
 RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,  
 RA Wolf Y.I., Hess W.R.;  
 RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,  
 RT a nearly minimal oxyphototrophic genome.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).  
 DR EMBL; AE017164; AAQ00225.1; -;  
 KW Complete proteome.  
 SQ SEQUENCE 88 AA; 9821 MW; D922EEC9BF6AE2F7 CRC64;  
 Query Match 100.0%; Score 23; DB 16; Length 88;  
 Best Local Similarity 100.0%; Pred. NO. 3.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DAHK 4  
 Db 74 DAHK 77

Search completed: September 9, 2004, 23:47:56  
 Job time : 154 secs

Fri Sep 10 11:38:08 2004

us-10-076-071-1.rag

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 9, 2004, 23:32:32 ; Search time 125 Seconds  
(without alignments)  
9.042 Million cell updates/sec

Title: US-10-076-071-1

Perfect score: 23  
Sequence: 1 DAHX 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : A\_Geneseq\_29Jan04.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1990s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	4	3 AAY90711	Aay90711 Human alb
2	23	100.0	4	4 AAB74365	Aab74365 Reactive
3	23	100.0	4	4 AAB86898	Aab86898 Transport
4	23	100.0	4	5 AAE14799	Aae14799 Human ser
5	23	100.0	4	6 ABR39034	Abr39034 Acylated
6	23	100.0	4	6 ABP98620	Abp98620 Cu-chelat
7	23	100.0	4	6 ABP98473	Abp98473 Amino aci
8	23	100.0	5	6 ABR39023	Abr39023 Acylated
9	23	100.0	6	2 AAW23611	Aaw23611 Prolactin
10	23	100.0	6	2 AAW23634	Aaw23634 Human pro
11	23	100.0	7	6 ABR39046	Abr39046 Acylated
12	23	100.0	8	3 AAY90712	Aay90712 Human alb
13	23	100.0	8	5 ABG70867	Abg70867 Fluoresce
14	23	100.0	9	4 AAE13134	Aae13134 Human alb
15	23	100.0	9	6 ABR39047	Abr39047 Acylated
16	23	100.0	10	4 AAG96326	Aag96326 Human com
17	23	100.0	10	4 AAG96328	Aag96328 Human com
18	23	100.0	11	6 ABR39048	Abr39048 Acylated
19	23	100.0	12	2 AAR37401	Aar37401 Human ser
20	23	100.0	12	4 AAB74367	Aab74367 Reactive
21	23	100.0	12	4 AAB74370	Aab74370 Reactive
22	23	100.0	12	5 AAE14804	Aae14804 Human rea
23	23	100.0	12	5 AAE14801	Aae14801 Human rea
24	23	100.0	12	6 ABB99709	Abb99709 Biopolyme
25	23	100.0	13	6 ABG75657	Abg75657 Congestiv

26	23	100.0	14	6 ABU08831	Abu08831 Serum alb
27	23	100.0	15	6 ABU08835	Abu08835 Serum alb
28	23	100.0	15	6 ABU09403	Abu09403 Renal fai
29	23	100.0	17	7 ADB61646	Adb61646 Human syn
30	23	100.0	20	3 AAB12462	Aab12462 Human alb
31	23	100.0	24	2 AAR80304	Aar80304 Invertase
32	23	100.0	24	2 AAO20109	Aao20109 24-mer pe
33	23	100.0	24	4 AAM52566	Aam52566 Peptide c
34	23	100.0	24	4 AAE12402	Aae12402 Fusion pe
35	23	100.0	24	4 AAE13128	Aae13128 Fusion pe
36	23	100.0	24	4 AAE13398	Aae13398 Fusion pe
37	23	100.0	24	4 AAB79005	Abb79005 Human alb
38	23	100.0	24	5 AAU75219	Aau75219 SUC2 lead
39	23	100.0	24	5 ABG63320	Abg63320 S. cerevi
40	23	100.0	24	6 ABR55694	Abr55694 Invertase
41	23	100.0	24	7 ADD68005	Add68005 Yeast inv
42	23	100.0	26	2 AAR37995	Aar37995 Aspergill
43	23	100.0	26	6 ABU08846	Abu08846 Serum alb
44	23	100.0	26	6 ABG75942	Abg75942 Human ser
45	23	100.0	28	6 ABU08847	Abu08847 Serum alb
46	23	100.0	28	6 ABU09223	Abu09223 Serum alb
47	23	100.0	32	4 AAB98752	Aab98752 Human sec
48	23	100.0	32	4 AAB98799	Aab98799 Human sec
49	23	100.0	37	4 AAB84272	Aab84272 Secondary
50	23	100.0	38	6 ABF78795	Abp78795 N. gonorr
51	23	100.0	41	4 AAB98822	Aab98822 Human sec
52	23	100.0	41	4 AAB98777	Aab98777 Human sec
53	23	100.0	41	4 AAB84292	Aab84292 Amino aci
54	23	100.0	42	3 AAB12839	Aab12839 Protein k
55	23	100.0	47	4 AAO09023	Aao09023 Human pol
56	23	100.0	53	4 AAM18531	Aam18531 Peptide #
57	23	100.0	53	4 ABB37566	Abb37566 Peptide #
58	23	100.0	53	4 AAM30988	Aam30988 Peptide #
59	23	100.0	53	4 ABB32307	Abb32307 Peptide #
60	23	100.0	53	4 ABB22861	Abb22861 Protein #
61	23	100.0	53	4 AAM70677	Aam70677 Human bon
62	23	100.0	53	4 AAM58223	Aam58223 Human bra
63	23	100.0	53	4 ABG52381	Abg52381 Human liv
64	23	100.0	53	4 AAM06099	Aam06099 Peptide #
65	23	100.0	53	5 ABG40382	Abg40382 Human pep
66	23	100.0	54	4 ABB14996	Abb14996 Human ner
67	23	100.0	55	3 AAG58879	Aag58879 Arabidops
68	23	100.0	57	5 AAE19578	Aae19578 Equine he
69	23	100.0	60	5 ABP10253	Abp10253 Human ORF
70	23	100.0	65	4 AAM91854	Aam91854 Human imm
71	23	100.0	67	5 AAB10998	Abp10998 Human ORF
72	23	100.0	72	5 ABP35027	Abp35027 Human tra
73	23	100.0	73	5 ABP34960	Abp34960 Human ORF
74	23	100.0	87	6 ABP79101	Abp79101 N. gonorr
75	23	100.0	90	4 ABG03214	Abg03214 Novel hum
76	23	100.0	92	5 ABP41442	Abp41442 Human ova
77	23	100.0	94	4 AAM84542	Aam84542 Human imm
78	23	100.0	96	5 ABP63825	Abp63825 Human ORF
79	23	100.0	97	4 AAO03583	Aao03583 Human pol
80	23	100.0	100	5 ABB54788	Abb54788 Lactococc
81	23	100.0	104	4 ABB03321	Abb03321 Human mus
82	23	100.0	104	4 ABB29873	Aab29873 Novel hum
83	23	100.0	104	6 ABU12615	Abu12615 Novel hum
84	23	100.0	104	6 ABU28386	Abu28386 Protein e
85	23	100.0	113	4 AAO11631	Aao11631 Human pol
86	23	100.0	114	3 AAB32825	Aab32825 Eucalyptu
87	23	100.0	114	4 AAU46378	Aau46378 Propionib
88	23	100.0	114	6 ABM42897	Abm42897 Propionib
89	23	100.0	116	4 AAO2642	Aao2642 Human pol
90	23	100.0	117	4 AAO16493	Aao16493 Human nov
91	23	100.0	117	4 AAM42255	Aam42255 Human bre
92	23	100.0	117	4 AAM94448	Aam94448 Human rep
93	23	100.0	117	6 AAM55562	Aam55562 Human nov
94	23	100.0	119	4 AAO11632	Aao11632 Human pol
95	23	100.0	120	4 ABG18807	Abg18807 Novel hum
96	23	100.0	121	4 AAU16064	Aau16064 Human nov
97	23	100.0	121	6 ABU55133	Abu55133 Human nov

99	23	100.0	123	4	AAO04424	Aao04424 Human pol	172	23	100.0	240	4	AAW94259	Aam94259 Human rep
100	23	100.0	124	4	AAO02630	Aao02630 Human pol	173	23	100.0	241	5	AAO16984	Aao16984 Alpha-MSH
101	23	100.0	124	4	AAO10348	Aao10348 Human pol	174	23	100.0	241	7	ABU10025	Abu10025 Alpha-MSH
102	23	100.0	125	3	AB411211	Ab411211 Human ORF	175	23	100.0	242	5	AAO16985	Aao16985 Alpha-MSH
103	23	100.0	127	4	AB63041	Ab63041 Drosophil	176	23	100.0	244	4	AB65124	Ab65124 Drosophil
104	23	100.0	128	4	AB633248	Ab633248 Drosophil	177	23	100.0	244	5	AAO16986	Aao16986 Alpha-MSH
105	23	100.0	132	4	AAO09589	Aao09589 Human pol	178	23	100.0	245	3	AAO23055	Aao23055 Arabidops
106	23	100.0	133	1	AAO09589	Aao09589 Human pol	179	23	100.0	245	4	AAO23055	Aao23055 Arabidops
107	23	100.0	133	1	AAO09589	Aao09589 Human pol	180	23	100.0	245	4	AAO23055	Aao23055 Arabidops
108	23	100.0	134	3	AAO16390	Aao16390 Pinus rad	181	23	100.0	245	5	AAO16987	Aao16987 Alpha-MSH
109	23	100.0	134	3	AAO16390	Aao16390 Pinus rad	182	23	100.0	245	5	AAO16988	Aao16988 Alpha-MSH
110	23	100.0	137	4	AAO12088	Aao12088 Human pol	183	23	100.0	247	4	AAU37676	Aau37676 Streptoco
111	23	100.0	138	5	ABP39993	Abp39993 Staphyloc	184	23	100.0	248	4	AAO07979	Aao07979 Human pol
112	23	100.0	141	6	ABP79507	Abp79507 N. gonorr	185	23	100.0	249	4	AB69435	Ab69435 Drosophil
113	23	100.0	142	4	AAO07915	Aao07915 C. albican	186	23	100.0	252	5	ABU51265	Abu51265 Helicobac
114	23	100.0	144	6	ADA36505	Ada36505 Acinetoba	187	23	100.0	259	5	ABU51009	Abu51009 Helicobac
115	23	100.0	145	4	ABG20922	Abg20922 Novel hum	188	23	100.0	259	5	ABU51792	Abu51792 Helicobac
116	23	100.0	148	5	ABP42171	Abp42171 Human ova	189	23	100.0	263	3	AAO09863	Aao09863 Arabidops
117	23	100.0	149	6	ABM65278	Abm65278 Propionib	190	23	100.0	263	5	AAU74729	Aau74729 Arabidops
118	23	100.0	153	4	AAO10773	Aao10773 Human pol	191	23	100.0	267	2	AAW61029	Aaw61029 Human gua
119	23	100.0	155	4	AAO10773	Aao10773 Human pol	192	23	100.0	267	5	AAO16989	Aao16989 Alpha-MSH
120	23	100.0	159	5	AB80777	Ab80777 A. salmon	193	23	100.0	268	7	ABU10026	Abu10026 Alpha-MSH
121	23	100.0	160	2	AAO33386	Aao33386 Max prote	194	23	100.0	268	5	ABU10026	Abu10026 Alpha-MSH
122	23	100.0	165	3	AAO33386	Aao33386 Max prote	195	23	100.0	270	5	ABU51448	Abu51448 Helicobac
123	23	100.0	166	3	AAO33386	Aao33386 Max prote	196	23	100.0	270	5	ABU52203	Abu52203 Helicobac
124	23	100.0	168	4	AAO33386	Aao33386 Max prote	197	23	100.0	271	3	AAO49856	Aao49856 Arabidops
125	23	100.0	168	4	AAO33386	Aao33386 Max prote	198	23	100.0	271	3	AAO49856	Aao49856 Arabidops
126	23	100.0	168	4	AAO33386	Aao33386 Max prote	199	23	100.0	271	6	ABU24847	Abu24847 Arabidops
127	23	100.0	172	2	AAO33386	Aao33386 Max prote	200	23	100.0	271	6	ABU24847	Abu24847 Arabidops
128	23	100.0	173	6	AAO33386	Aao33386 Max prote	201	23	100.0	274	2	AAO35779	Aao35779 Acinetoba
129	23	100.0	175	6	AAO33386	Aao33386 Max prote	202	23	100.0	276	2	AAO35779	Aao35779 Acinetoba
130	23	100.0	175	6	AAO33386	Aao33386 Max prote	203	23	100.0	276	2	AAO35779	Aao35779 Acinetoba
131	23	100.0	177	4	AAO33386	Aao33386 Max prote	204	23	100.0	276	5	AAO35779	Aao35779 Acinetoba
132	23	100.0	178	6	AAO33386	Aao33386 Max prote	205	23	100.0	276	5	AAO35779	Aao35779 Acinetoba
133	23	100.0	181	6	AAO33386	Aao33386 Max prote	206	23	100.0	276	5	AAO35779	Aao35779 Acinetoba
134	23	100.0	182	2	AAO33386	Aao33386 Max prote	207	23	100.0	277	2	AAO35779	Aao35779 Acinetoba
135	23	100.0	184	4	AAO33386	Aao33386 Max prote	208	23	100.0	277	2	AAO35779	Aao35779 Acinetoba
136	23	100.0	184	4	AAO33386	Aao33386 Max prote	209	23	100.0	277	2	AAO35779	Aao35779 Acinetoba
137	23	100.0	186	3	AAO33386	Aao33386 Max prote	210	23	100.0	277	4	AAO35779	Aao35779 Acinetoba
138	23	100.0	186	3	AAO33386	Aao33386 Max prote	211	23	100.0	277	6	AAO35779	Aao35779 Acinetoba
139	23	100.0	187	6	AAO33386	Aao33386 Max prote	212	23	100.0	277	6	AAO35779	Aao35779 Acinetoba
140	23	100.0	190	4	AAO33386	Aao33386 Max prote	213	23	100.0	277	6	AAO35779	Aao35779 Acinetoba
141	23	100.0	192	4	AAO33386	Aao33386 Max prote	214	23	100.0	277	7	AAO35779	Aao35779 Acinetoba
142	23	100.0	195	5	AAO33386	Aao33386 Max prote	215	23	100.0	278	3	AAO35779	Aao35779 Acinetoba
143	23	100.0	195	6	AAO33386	Aao33386 Max prote	216	23	100.0	278	3	AAO35779	Aao35779 Acinetoba
144	23	100.0	196	5	AAO33386	Aao33386 Max prote	217	23	100.0	280	2	AAO35779	Aao35779 Acinetoba
145	23	100.0	196	5	AAO33386	Aao33386 Max prote	218	23	100.0	280	2	AAO35779	Aao35779 Acinetoba
146	23	100.0	200	6	AAO33386	Aao33386 Max prote	219	23	100.0	280	3	AAO35779	Aao35779 Acinetoba
147	23	100.0	200	7	AAO33386	Aao33386 Max prote	220	23	100.0	280	3	AAO35779	Aao35779 Acinetoba
148	23	100.0	204	3	AAO33386	Aao33386 Max prote	221	23	100.0	280	5	AAO35779	Aao35779 Acinetoba
149	23	100.0	205	4	AAO33386	Aao33386 Max prote	222	23	100.0	280	5	AAO35779	Aao35779 Acinetoba
150	23	100.0	214	4	AAO33386	Aao33386 Max prote	223	23	100.0	280	5	AAO35779	Aao35779 Acinetoba
151	23	100.0	218	6	AAO33386	Aao33386 Max prote	224	23	100.0	280	5	AAO35779	Aao35779 Acinetoba
152	23	100.0	219	3	AAO33386	Aao33386 Max prote	225	23	100.0	280	6	AAO35779	Aao35779 Acinetoba
153	23	100.0	222	6	AAO33386	Aao33386 Max prote	226	23	100.0	288	5	AAO35779	Aao35779 Acinetoba
154	23	100.0	222	6	AAO33386	Aao33386 Max prote	227	23	100.0	288	5	AAO35779	Aao35779 Acinetoba
155	23	100.0	222	6	AAO33386	Aao33386 Max prote	228	23	100.0	288	5	AAO35779	Aao35779 Acinetoba
156	23	100.0	223	6	AAO33386	Aao33386 Max prote	229	23	100.0	288	5	AAO35779	Aao35779 Acinetoba
157	23	100.0	224	6	AAO33386	Aao33386 Max prote	230	23	100.0	288	5	AAO35779	Aao35779 Acinetoba
158	23	100.0	227	6	AAO33386	Aao33386 Max prote	231	23	100.0	288	5	AAO35779	Aao35779 Acinetoba
159	23	100.0	231	5	AAO33386	Aao33386 Max prote	232	23	100.0	288	5	AAO35779	Aao35779 Acinetoba
160	23	100.0	231	5	AAO33386	Aao33386 Max prote	233	23	100.0	288	5	AAO35779	Aao35779 Acinetoba
161	23	100.0	231	5	AAO33386	Aao33386 Max prote	234	23	100.0	288	5	AAO35779	Aao35779 Acinetoba
162	23	100.0	232	2	AAO33386	Aao33386 Max prote	235	23	100.0	289	4	AAO35779	Aao35779 Acinetoba
163	23	100.0	233	2	AAO33386	Aao33386 Max prote	236	23	100.0	289	4	AAO35779	Aao35779 Acinetoba
164	23	100.0	233	2	AAO33386	Aao33386 Max prote	237	23	100.0	289	4	AAO35779	Aao35779 Acinetoba
165	23	100.0	234	3	AAO33386	Aao33386 Max prote	238	23	100.0	289	4	AAO35779	Aao35779 Acinetoba
166	23	100.0	234	3	AAO33386	Aao33386 Max prote	239	23	100.0	289	4	AAO35779	Aao35779 Acinetoba
167	23	100.0	234	3	AAO33386	Aao33386 Max prote	240	23	100.0	289	4	AAO35779	Aao35779 Acinetoba
168	23	100.0	236	5	AAO33386	Aao33386 Max prote	241	23	100.0	292	6	AAO35779	Aao35779 Acinetoba
169	23	100.0	237	5	AAO33386	Aao33386 Max prote	242	23	100.0	292	6	AAO35779	Aao35779 Acinetoba
170	23	100.0	238	5	AAO33386	Aao33386 Max prote	243	23	100.0	295	6	AAO35779	Aao35779 Acinetoba
171	23	100.0	239	3	AAO33386	Aao33386 Max prote	244	23	100.0	296	6	AAO35779	Aao35779 Acinetoba

245	23	100.0	298	2	AAW5683	Aaw95683	Saccharom	318	23	100.0	357	6	ABU43319	Abu43319	Protein e
246	23	100.0	298	3	AAG23054	Aag23054	Arabidops	319	23	100.0	357	6	ABU42597	Abu42597	Protein e
247	23	100.0	298	4	ABG84912	Abg84912	Shrimp wh	320	23	100.0	357	6	ABU43180	Abu43180	Protein e
248	23	100.0	298	5	ABR52995	AbR52995	Protein s	321	23	100.0	357	6	ABU42750	Abu42750	Protein e
249	23	100.0	300	4	ABB67446	Abb67446	Drosophil	322	23	100.0	357	6	ABU42643	Abu42643	Protein e
250	23	100.0	300	6	ABU21414	Abu21414	Protein e	323	23	100.0	357	6	ABU42584	Abu42584	Protein e
251	23	100.0	300	6	ABU21414	Abu21414	Protein e	324	23	100.0	357	6	ABU42775	Abu42775	Protein e
252	23	100.0	305	4	AAU34210	Aau34210	Human ser	325	23	100.0	358	5	ABB93911	Abb93911	Herbicida
253	23	100.0	306	3	AAU34210	Aau34210	Human pan	326	23	100.0	360	4	AAU35785	Aau35785	Helicobac
254	23	100.0	308	3	AAW60946	Aaw60946	Streptoco	327	23	100.0	360	6	ABU30899	Abu30899	Protein e
255	23	100.0	309	6	ABU33105	Abu33105	Protein e	328	23	100.0	361	3	AAU11129	Aag11129	Arabidops
256	23	100.0	312	7	ADC96057	Adc96057	E. faeciu	329	23	100.0	361	3	AAU46095	Aag46095	Arabidops
257	23	100.0	316	4	AAU87354	Aau87354	Novel cen	330	23	100.0	364	4	ABH60565	Abb60565	Drosophil
258	23	100.0	318	4	AAU87354	Aau87354	Novel cen	331	23	100.0	370	3	AAU46128	Aag46128	Arabidops
259	23	100.0	318	4	AAU87354	Aau87354	Novel cen	332	23	100.0	370	3	AAU46128	Aag46128	Arabidops
260	23	100.0	319	5	AAU99517	Aau99517	Protein e	333	23	100.0	370	3	AAU46128	Aag46128	Arabidops
261	23	100.0	324	4	AAU87354	Aau87354	Novel cen	334	23	100.0	370	3	AAU46128	Aag46128	Arabidops
262	23	100.0	325	3	AAU87354	Aau87354	Novel cen	335	23	100.0	370	3	AAU46128	Aag46128	Arabidops
263	23	100.0	325	3	AAU87354	Aau87354	Novel cen	336	23	100.0	370	3	AAU46128	Aag46128	Arabidops
264	23	100.0	325	6	ABP76742	Abp76742	N. gonorr	337	23	100.0	375	5	ABP39073	Abp39073	Staphyloc
265	23	100.0	325	6	ABP76742	Abp76742	N. gonorr	338	23	100.0	378	4	AAU17063	Aau17063	Human pol
266	23	100.0	326	4	AAU87354	Aau87354	Novel cen	339	23	100.0	378	4	AAU17063	Aau17063	Human pol
267	23	100.0	326	4	AAU87354	Aau87354	Novel cen	340	23	100.0	378	4	AAU17063	Aau17063	Human pol
268	23	100.0	328	3	AAU87354	Aau87354	Novel cen	341	23	100.0	378	4	AAU17063	Aau17063	Human pol
269	23	100.0	329	3	AAU87354	Aau87354	Novel cen	342	23	100.0	378	4	AAU17063	Aau17063	Human pol
270	23	100.0	329	3	AAU87354	Aau87354	Novel cen	343	23	100.0	378	4	AAU17063	Aau17063	Human pol
271	23	100.0	329	3	AAU87354	Aau87354	Novel cen	344	23	100.0	378	4	AAU17063	Aau17063	Human pol
272	23	100.0	329	4	AAU87354	Aau87354	Novel cen	345	23	100.0	378	4	AAU17063	Aau17063	Human pol
273	23	100.0	330	4	AAU87354	Aau87354	Novel cen	346	23	100.0	378	4	AAU17063	Aau17063	Human pol
274	23	100.0	330	4	AAU87354	Aau87354	Novel cen	347	23	100.0	378	4	AAU17063	Aau17063	Human pol
275	23	100.0	330	4	AAU87354	Aau87354	Novel cen	348	23	100.0	378	4	AAU17063	Aau17063	Human pol
276	23	100.0	330	6	ABU01586	Abu01586	S. pneumo	349	23	100.0	389	1	AAF90390	Aap90390	N-termina
277	23	100.0	330	6	ABU01586	Abu01586	S. pneumo	350	23	100.0	390	1	AAF90390	Aap90390	N-termina
278	23	100.0	330	6	ABU01586	Abu01586	S. pneumo	351	23	100.0	390	1	AAF90390	Aap90390	N-termina
279	23	100.0	336	5	ABP65202	Abp65202	Hypoxia-r	352	23	100.0	390	1	AAF90390	Aap90390	N-termina
280	23	100.0	336	5	ABP65202	Abp65202	Hypoxia-r	353	23	100.0	390	1	AAF90390	Aap90390	N-termina
281	23	100.0	336	6	ABU49401	Abu49401	Protein e	354	23	100.0	394	4	ABP76621	Abp76621	Corynebac
282	23	100.0	337	4	AAU87354	Aau87354	Novel cen	355	23	100.0	394	4	ABP76621	Abp76621	Corynebac
283	23	100.0	337	4	AAU87354	Aau87354	Novel cen	356	23	100.0	394	4	ABP76621	Abp76621	Corynebac
284	23	100.0	337	4	AAU87354	Aau87354	Novel cen	357	23	100.0	400	7	ADC95048	Adc95048	E. faeciu
285	23	100.0	337	4	AAU87354	Aau87354	Novel cen	358	23	100.0	400	7	ADC95048	Adc95048	E. faeciu
286	23	100.0	337	4	AAU87354	Aau87354	Novel cen	359	23	100.0	400	7	ADC95048	Adc95048	E. faeciu
287	23	100.0	337	4	AAU87354	Aau87354	Novel cen	360	23	100.0	401	4	AAU29876	Aau29876	Novel hum
288	23	100.0	337	4	AAU87354	Aau87354	Novel cen	361	23	100.0	401	4	AAU29876	Aau29876	Novel hum
289	23	100.0	337	4	AAU87354	Aau87354	Novel cen	362	23	100.0	401	4	AAU29876	Aau29876	Novel hum
290	23	100.0	337	4	AAU87354	Aau87354	Novel cen	363	23	100.0	401	4	AAU29876	Aau29876	Novel hum
291	23	100.0	337	4	AAU87354	Aau87354	Novel cen	364	23	100.0	401	4	AAU29876	Aau29876	Novel hum
292	23	100.0	337	4	AAU87354	Aau87354	Novel cen	365	23	100.0	401	4	AAU29876	Aau29876	Novel hum
293	23	100.0	337	7	AAU87354	Aau87354	Novel cen	366	23	100.0	401	4	AAU29876	Aau29876	Novel hum
294	23	100.0	337	7	AAU87354	Aau87354	Novel cen	367	23	100.0	401	4	AAU29876	Aau29876	Novel hum
295	23	100.0	337	7	AAU87354	Aau87354	Novel cen	368	23	100.0	401	4	AAU29876	Aau29876	Novel hum
296	23	100.0	337	7	AAU87354	Aau87354	Novel cen	369	23	100.0	401	4	AAU29876	Aau29876	Novel hum
297	23	100.0	337	7	AAU87354	Aau87354	Novel cen	370	23	100.0	401	4	AAU29876	Aau29876	Novel hum
298	23	100.0	337	7	AAU87354	Aau87354	Novel cen	371	23	100.0	401	4	AAU29876	Aau29876	Novel hum
299	23	100.0	340	4	ABU65378	Abu65378	Drosophil	372	23	100.0	401	4	AAU29876	Aau29876	Novel hum
300	23	100.0	340	4	AAU47013	Aau47013	Propionib	373	23	100.0	401	4	AAU29876	Aau29876	Novel hum
301	23	100.0	340	6	ABM43532	Abm43532	Human pro	374	23	100.0	401	4	AAU29876	Aau29876	Novel hum
302	23	100.0	342	5	ABP95647	Abp95647	Human GPC	375	23	100.0	401	4	AAU29876	Aau29876	Novel hum
303	23	100.0	343	6	ABO52948	AbO52948	Human spl	376	23	100.0	401	4	AAU29876	Aau29876	Novel hum
304	23	100.0	344	6	ABO52948	AbO52948	Human spl	377	23	100.0	401	4	AAU29876	Aau29876	Novel hum
305	23	100.0	345	6	ABR39092	AbR39092	Cercopith	378	23	100.0	401	4	AAU29876	Aau29876	Novel hum
306	23	100.0	345	6	ABR39092	AbR39092	Cercopith	379	23	100.0	401	4	AAU29876	Aau29876	Novel hum
307	23	100.0	345	6	ABR39092	AbR39092	Cercopith	380	23	100.0	401	4	AAU29876	Aau29876	Novel hum
308	23	100.0	347	6	AAU36873	Aau36873	Staphyloc	381	23	100.0	401	4	AAU29876	Aau29876	Novel hum
309	23	100.0	347	6	ABU16338	AbU16338	pathogen	382	23	100.0	401	4	AAU29876	Aau29876	Novel hum
310	23	100.0	347	6	ABU16338	AbU16338	pathogen	383	23	100.0	401	4	AAU29876	Aau29876	Novel hum
311	23	100.0	353	5	ABW75759	AbW75759	Physcomit	384	23	100.0	401	4	AAU29876	Aau29876	Novel hum
312	23	100.0	353	5	ABW75759	AbW75759	Physcomit	385	23	100.0	401	4	AAU29876	Aau29876	Novel hum
313	23	100.0	353	5	ABW75759	AbW75759	Physcomit	386	23	100.0	401	4	AAU29876	Aau29876	Novel hum
314	23	100.0	357	6	ABU43145	Abu43145	Protein e	387	23	100.0	401	4	AAU29876	Aau29876	Novel hum
315	23	100.0	357	6	ABU43145	Abu43145	Protein e	388	23	100.0	401	4	AAU29876	Aau29876	Novel hum
316	23	100.0	357	6	ABU42588	Abu42588	Protein e	389	23	100.0	401	4	AAU29876	Aau29876	Novel hum
317	23	100.0	357	6	ABU42588	Abu42588	Protein e	390	23	100.0	401	4	AAU29876	Aau29876	Novel hum

391	23	100.0	461	6	Abm69616	Phototrab	464	23	100.0	585	2	AAR05318	Human ser
392	23	100.0	461	6	Abm70151	Phototrab	465	23	100.0	585	2	AAR08457	Human ser
393	23	100.0	466	3	Agm46126	Arabidops	466	23	100.0	585	2	AAR26207	Human ser
394	23	100.0	466	3	Agm51772	Arabidops	467	23	100.0	585	2	AAR26362	Synthetic
395	23	100.0	467	5	Abp69216	Human pol	468	23	100.0	585	2	AAR20029	Human ser
396	23	100.0	467	5	Abp93938	Herbicida	469	23	100.0	585	2	AAR80301	Human ser
397	23	100.0	469	2	Aar22359	Histidino	470	23	100.0	585	2	AAR20111	HSA prote
398	23	100.0	469	4	Agm90154	C glutami	471	23	100.0	585	2	AAY59841	Mature pr
399	23	100.0	469	4	Abm73380	Moraxella	472	23	100.0	585	3	AAY84873	Amino aci
400	23	100.0	469	4	Abm83184	Corynebac	473	23	100.0	585	3	AAY83946	Yeast cod
401	23	100.0	470	5	Abm19560	Equine he	474	23	100.0	585	4	AAY2567	Mature hu
402	23	100.0	482	7	Abm78972	Arabidops	475	23	100.0	585	4	AAY12417	Human alb
403	23	100.0	484	2	Aam55720	H. pylori	476	23	100.0	585	4	AAY12403	Human alb
404	23	100.0	484	2	Aam55700	H. pylori	477	23	100.0	585	4	AAY13129	Human alb
405	23	100.0	484	2	Aam98826	H. pylori	478	23	100.0	585	4	AAY13135	Human alb
406	23	100.0	484	6	Abu38941	Protein e	479	23	100.0	585	4	AAY13311	Human alb
407	23	100.0	485	2	Aam23245	Human ang	480	23	100.0	585	4	AAY13399	Human alb
408	23	100.0	485	4	Aab48945	Human ang	481	23	100.0	585	4	Abm79006	Human mat
409	23	100.0	485	4	Aab48944	Human ang	482	23	100.0	585	4	Abm79006	Human mat
410	23	100.0	485	4	Aab48949	Human ang	483	23	100.0	585	4	Abm79006	Human mat
411	23	100.0	485	4	Aab48947	Human ang	484	23	100.0	585	5	Aau75220	Mature fo
412	23	100.0	485	4	Aab48946	Human ang	485	23	100.0	585	5	Abj00986	B lymphoc
413	23	100.0	485	4	Aab48948	Human ang	486	23	100.0	585	5	Abg63321	Human ser
414	23	100.0	485	4	Aab67350	Human ang	487	23	100.0	585	5	Abg633847	Human B.L
415	23	100.0	485	4	Aau31120	Novel hum	488	23	100.0	585	5	Abg71231	Glycosyla
416	23	100.0	489	5	Abp38075	Staphyloc	489	23	100.0	585	6	Abg72380	Mature hu
417	23	100.0	491	6	Abm69741	Phototrab	490	23	100.0	585	6	Abm72380	Mature hu
418	23	100.0	494	4	Abm71469	Arabidops	491	23	100.0	585	6	Abm72380	Mature hu
419	23	100.0	494	4	Abm68783	Drosophil	492	23	100.0	585	7	Abm72380	Mature hu
420	23	100.0	494	4	Abm71945	Drosophil	493	23	100.0	585	7	Abm72380	Mature hu
421	23	100.0	494	6	Abm72676	Drosophil	494	23	100.0	585	7	Abm72380	Mature hu
422	23	100.0	496	5	Aao26369	Human spl	495	23	100.0	585	7	Abm72380	Mature hu
423	23	100.0	500	6	Abu26688	Protein e	496	23	100.0	585	7	Abm72380	Mature hu
424	23	100.0	500	7	Add32019	Heterolog	497	23	100.0	585	7	Abm72380	Mature hu
425	23	100.0	501	6	Abm68457	Phototrab	498	23	100.0	586	1	AAP60072	Sequence
426	23	100.0	505	2	Aam61027	Murine gu	499	23	100.0	586	1	AAP60072	Sequence
427	23	100.0	507	4	Abm71378	Drosophil	500	23	100.0	586	1	AAP60839	Sequence
428	23	100.0	507	4	Abm71378	Drosophil	501	23	100.0	586	1	AAP70767	Human ser
429	23	100.0	507	4	Agm80043	Pseudomon	502	23	100.0	588	2	AAR13021	HSA-liver
430	23	100.0	507	4	Agm80035	Pseudomon	503	23	100.0	590	2	AAR12558	HSA-fibro
431	23	100.0	508	2	Aam64772	Serine th	504	23	100.0	590	2	AAR12558	HSA-fibro
432	23	100.0	508	4	Abm60795	Drosophil	505	23	100.0	591	4	Abg29309	HSA-nucle
433	23	100.0	508	4	Abm72676	Drosophil	506	23	100.0	598	4	Abm72676	Drosophil
434	23	100.0	510	2	Aay35221	Drosophil	507	23	100.0	598	4	Abm72676	Drosophil
435	23	100.0	510	6	Abu30442	Chlamydia	508	23	100.0	598	4	Abm72676	Drosophil
436	23	100.0	517	4	Abm70723	Protein e	509	23	100.0	608	2	AAR04223	Sequence
437	23	100.0	520	2	Aam36491	Human TUL	510	23	100.0	608	2	AAR05784	Fragment
438	23	100.0	520	3	Abm26906	Human TUL	511	23	100.0	608	2	AAR96229	Human ser
439	23	100.0	523	4	Abm65104	Drosophil	512	23	100.0	609	1	AAP30089	Sequence
440	23	100.0	531	6	Abm14652	Novel hum	513	23	100.0	609	1	AAP30188	Sequence
441	23	100.0	534	5	Abm90805	Human she	514	23	100.0	609	1	AAP60092	Sequence
442	23	100.0	534	5	Aao26364	Human EHD	515	23	100.0	609	1	AAP60092	Sequence
443	23	100.0	534	5	Aao26365	Mouse EHD	516	23	100.0	609	1	AAP60064	Recombina
444	23	100.0	535	2	Aam61028	Murine gu	517	23	100.0	609	2	AAR27860	HSA: 3/20
445	23	100.0	535	2	Aam61028	Murine gu	518	23	100.0	609	2	AAR25309	HSA: 3/20
446	23	100.0	535	4	Aam40305	Human pol	519	23	100.0	609	2	AAR32563	HSA: 3/20
447	23	100.0	535	5	Aao26368	EHD1 deri	520	23	100.0	609	2	AAR94572	Cancer me
448	23	100.0	535	5	Aao26367	Mouse EHD	521	23	100.0	609	2	AAR8913	Human ser
449	23	100.0	535	6	Abm78251	N. gonorr	522	23	100.0	609	2	AAR96232	Human ser
450	23	100.0	538	6	Abm78251	N. gonorr	523	23	100.0	609	2	AAR96232	Human ser
451	23	100.0	541	7	Abm78251	N. gonorr	524	23	100.0	609	3	AAY60994	Human alb
452	23	100.0	543	5	Abm64897	Human pro	525	23	100.0	609	3	AAY60994	Human alb
453	23	100.0	546	4	Abm64897	Human pro	526	23	100.0	609	3	AAY60994	Human alb
454	23	100.0	550	4	Abm64897	Human pro	527	23	100.0	609	3	AAY60994	Human alb
455	23	100.0	554	2	Aam61026	Murine gu	528	23	100.0	609	3	AAY60994	Human alb
456	23	100.0	562	6	Abm26699	Protein e	529	23	100.0	609	3	AAY60994	Human alb
457	23	100.0	564	4	Abm94597	Human pro	530	23	100.0	609	7	Abm94597	Human pro
458	23	100.0	573	5	Abm70153	Human pro	531	23	100.0	609	7	Abm94597	Human pro
459	23	100.0	583	4	Abm30814	Novel hum	532	23	100.0	609	8	Abm94597	Human pro
460	23	100.0	584	6	Abm72381	Mature hu	533	23	100.0	610	2	AAR96232	Human ser
461	23	100.0	585	1	AAP93344	Sequence	534	23	100.0	615	6	Abu21184	Protein e
462	23	100.0	585	1	AAP90388	Mature hu	535	23	100.0	616	6	Abu19688	Protein e
463	23	100.0	585	1	AAP91422	Human nor	536	23	100.0	616	6	Abu19688	Protein e

537	23	100.0	618	7	ADD71142	Adg71142 Human int	610	23	100.0	750	4	AAU29878	Aau29878 Novel hum
538	23	100.0	620	6	ABP98783	Abp98783 Full leng	611	23	100.0	750	4	AAU29881	Aau29881 Novel hum
539	23	100.0	621	2	AAR37870	Aar37870 Soluble K	612	23	100.0	750	6	ABU47656	Abu47656 Protein e
540	23	100.0	622	2	AAR20469	Aar20469 Soluble Y	613	23	100.0	753	4	AAR34588	Aar34588 E. coli c
541	23	100.0	623	5	ABB77434	Abb77434 Human tum	614	23	100.0	753	6	ABU14954	Abu14954 Protein e
542	23	100.0	624	5	ABB55583	Abb55583 Lactococc	615	23	100.0	754	2	AAR92149	Aar92149 HSA:Fc ga
543	23	100.0	624	6	AAE30919	Aae30919 Human ser	616	23	100.0	765	4	ABG28515	Abg28515 Novel hum
544	23	100.0	625	4	ABBS5896	Abbs5896 Drosophil	617	23	100.0	766	4	ABU53068	Abu53068 Transport
545	23	100.0	630	4	AAU93102	Aau93102 Human pro	618	23	100.0	779	6	ABR83434	AbR83434 HSA-TIMP2
546	23	100.0	631	2	AAR96230	Aar96230 Human ser	619	23	100.0	783	2	AAR39473	Aar39473 Prepro-HS
547	23	100.0	631	4	ABBS65808	Abbs65808 Drosophil	620	23	100.0	787	2	AAR39477	Aar39477 G-CSF-(Gl
548	23	100.0	631	6	AAE30917	Aae30917 Val8-GLP-	621	23	100.0	789	4	AAU29880	Aau29880 Novel hum
549	23	100.0	632	2	AAE3096231	Aae3096231 Human ser	622	23	100.0	789	7	ADBE63953	Adbe63953 Rat Prote
550	23	100.0	635	4	ABR71475	AbR71475 Drosophil	623	23	100.0	791	3	ABY75756	AbY75756 Neisseria
551	23	100.0	639	6	AAU20668	Aau20668 Protein e	624	23	100.0	791	6	ABP79242	AbP79242 N. gonorr
552	23	100.0	640	6	AAE30920	Aae30920 Extensin-4	625	23	100.0	792	3	AAU75754	Aau75754 Neisseria
553	23	100.0	640	6	AAE30918	Aae30918 Gly8-Glu2	626	23	100.0	796	5	AAU66076	Aau66076 N. mening
554	23	100.0	641	3	AAV75755	Aav75755 Neisseria	627	23	100.0	796	5	ABM70487	Abm70487 Photorhab
555	23	100.0	651	7	ADD06597	Add06597 Human Ckb	628	23	100.0	801	6	ABM95231	Abm95231 Human pro
556	23	100.0	652	7	ADD06563	Add06563 Human Ckb	629	23	100.0	802	4	ABM95231	Abm95231 Human pro
557	23	100.0	652	7	ADD06596	Add06596 Human Ckb	630	23	100.0	810	4	AGS81232	AgS81232 Mycobacte
558	23	100.0	652	7	ADD06596	Add06596 Human Ckb	631	23	100.0	814	1	AAU90681	Aau90681 KEX2 endo
559	23	100.0	653	7	ADD06595	Add06595 Human Ckb	632	23	100.0	814	1	AAU90681	Aau90681 KEX2 endo
560	23	100.0	656	7	ADD06594	Add06594 Human Ckb	633	23	100.0	815	6	ADA32997	Ada32997 Acinetoba
561	23	100.0	656	7	ADD06594	Add06594 Human Ckb	634	23	100.0	823	4	ABG25584	Abg25584 Novel hum
562	23	100.0	659	7	ADCL6791	Adcl6791 Chimeric	635	23	100.0	825	6	ABM68441	Abm68441 Photorhab
563	23	100.0	659	7	ADCL6793	Adcl6793 Chimeric	636	23	100.0	830	6	ABM68441	Abm68441 Photorhab
564	23	100.0	660	7	ADD06557	Add06557 Human Ckb	637	23	100.0	835	2	AAR39472	Aar39472 HSA-vWF(4
565	23	100.0	660	7	ADD06554	Add06554 Human Ckb	638	23	100.0	853	2	AAR39472	Aar39472 HSA-vWF(4
566	23	100.0	662	7	ADCL6789	Adcl6789 Chimeric	639	23	100.0	865	6	ABU03216	Abu03216 Protein e
567	23	100.0	662	7	ADCL6787	Adcl6787 Chimeric	640	23	100.0	865	6	ABU14972	Abu14972 Protein e
568	23	100.0	668	4	ABR94411	AbR94411 Human pro	641	23	100.0	868	4	ABR62535	AbR62535 Drosophil
569	23	100.0	668	5	ABBS4996	Abbs4996 Lactococc	642	23	100.0	871	6	ABU26316	Abu26316 Protein e
570	23	100.0	668	6	ABU44992	Abu44992 Protein e	643	23	100.0	876	6	ABU49402	Abu49402 Protein e
571	23	100.0	668	7	ADD06566	Add06566 Human Ckb	644	23	100.0	879	4	AAU29879	Aau29879 Novel hum
572	23	100.0	670	3	AAAB36543	AaB36543 Recombina	645	23	100.0	883	2	AAU29879	Aau29879 Novel hum
573	23	100.0	670	3	AAAB36550	AaB36550 Recombina	646	23	100.0	883	2	AAU29879	Aau29879 Novel hum
574	23	100.0	671	5	ABF51430	AbF51430 Human MDD	647	23	100.0	883	2	AAU29879	Aau29879 Novel hum
575	23	100.0	672	7	ABR42610	AbR42610 Fusion pr	648	23	100.0	883	2	AAU29879	Aau29879 Novel hum
576	23	100.0	674	7	ABR42609	AbR42609 Fusion pr	649	23	100.0	883	2	AAU29879	Aau29879 Novel hum
577	23	100.0	676	4	ABBS8042	Abbs8042 Drosophil	650	23	100.0	883	2	AAU29879	Aau29879 Novel hum
578	23	100.0	676	7	ADD06591	Add06591 Human Ckb	651	23	100.0	883	2	AAU29879	Aau29879 Novel hum
579	23	100.0	676	7	ADD06568	Add06568 Human Ckb	652	23	100.0	883	2	AAU29879	Aau29879 Novel hum
580	23	100.0	676	7	ADD06559	Add06559 Human Ckb	653	23	100.0	883	2	AAU29879	Aau29879 Novel hum
581	23	100.0	676	7	ADD06552	Add06552 Human Ckb	654	23	100.0	883	2	AAU29879	Aau29879 Novel hum
582	23	100.0	677	7	ADD06593	Add06593 Human Ckb	655	23	100.0	883	2	AAU29879	Aau29879 Novel hum
583	23	100.0	677	7	ADD06589	Add06589 Human Ckb	656	23	100.0	883	2	AAU29879	Aau29879 Novel hum
584	23	100.0	680	7	ADD06587	Add06587 Human Ckb	657	23	100.0	883	2	AAU29879	Aau29879 Novel hum
585	23	100.0	684	4	AAU33090	Aau33090 Novel hum	658	23	100.0	883	2	AAU29879	Aau29879 Novel hum
586	23	100.0	684	7	ADD06556	Add06556 Human Ckb	659	23	100.0	883	2	AAU29879	Aau29879 Novel hum
587	23	100.0	687	7	ABR42612	AbR42612 Fusion pr	660	23	100.0	883	2	AAU29879	Aau29879 Novel hum
588	23	100.0	688	7	ABR42613	AbR42613 Fusion pr	661	23	100.0	883	2	AAU29879	Aau29879 Novel hum
589	23	100.0	689	7	ABR42608	AbR42608 Fusion pr	662	23	100.0	883	2	AAU29879	Aau29879 Novel hum
590	23	100.0	692	7	ADD06565	Add06565 Human Ckb	663	23	100.0	883	2	AAU29879	Aau29879 Novel hum
591	23	100.0	696	4	ABBS1108	Abbs1108 Drosophil	664	23	100.0	883	2	AAU29879	Aau29879 Novel hum
592	23	100.0	701	4	AAU94767	Aau94767 Human pro	665	23	100.0	883	2	AAU29879	Aau29879 Novel hum
593	23	100.0	702	4	AAU34524	Aau34524 E. coli c	666	23	100.0	883	2	AAU29879	Aau29879 Novel hum
594	23	100.0	703	5	ABBS3466	Abbs3466 Herbicida	667	23	100.0	883	2	AAU29879	Aau29879 Novel hum
595	23	100.0	710	2	AAW80995	Aaw80995 Human gua	668	23	100.0	883	2	AAU29879	Aau29879 Novel hum
596	23	100.0	711	6	AAU39585	Aau39585 Protein e	669	23	100.0	883	2	AAU29879	Aau29879 Novel hum
597	23	100.0	712	2	AAU20468	Aau20468 KEX2 endo	670	23	100.0	883	2	AAU29879	Aau29879 Novel hum
598	23	100.0	714	5	ABG33810	Abg33810 Transcrip	671	23	100.0	883	2	AAU29879	Aau29879 Novel hum
599	23	100.0	714	5	AAU71801	Aau71801 Zinc fing	672	23	100.0	883	2	AAU29879	Aau29879 Novel hum
600	23	100.0	718	2	AAU12560	Aau12560 HSA-IL-2	673	23	100.0	883	2	AAU29879	Aau29879 Novel hum
601	23	100.0	734	6	ABJ25384	Abj25384 Aspergill	674	23	100.0	883	2	AAU29879	Aau29879 Novel hum
602	23	100.0	736	5	AAU49042	Aau49042 Acaryochl	675	23	100.0	883	2	AAU29879	Aau29879 Novel hum
603	23	100.0	738	4	ABBS8451	Abbs8451 Drosophil	676	23	100.0	883	2	AAU29879	Aau29879 Novel hum
604	23	100.0	738	4	AAU38924	Aau38924 Drosophil	677	23	100.0	883	2	AAU29879	Aau29879 Novel hum
605	23	100.0	738	7	ADC35754	Adc35754 Drosophil	678	23	100.0	883	2	AAU29879	Aau29879 Novel hum
606	23	100.0	743	5	ABP35672	Abp35672 Fungal ZB	679	23	100.0	883	2	AAU29879	Aau29879 Novel hum
607	23	100.0	748	4	ABBS64114	Abbs64114 Drosophil	680	23	100.0	883	2	AAU29879	Aau29879 Novel hum
608	23	100.0	749	6	ABU27823	Abu27823 Protein e	681	23	100.0	883	2	AAU29879	Aau29879 Novel hum
609	23	100.0	750	4	AAU38392	Aau38392 Salmonell	682	23	100.0	883	2	AAU29879	Aau29879 Novel hum



683	23	100.0	1025	6	AAG79732	Agg79732 Rat IRAP.	756	20	87.0	7	ABR62810	AbR62810 9-G5 pept
684	23	100.0	1025	7	ADD48134	Add48134 Rat Prote	757	20	87.0	8	AAU03791	Aau03791 P21-activ
685	23	100.0	1026	2	AAR94511	Aar94511 GTVap (lo	758	20	87.0	8	ADBL17035	Adbl17035 Peptide s
686	23	100.0	1026	2	AAV43597	Aav43597 Amino aci	759	20	87.0	9	ADC44572	Adc44572 Endotheli
687	23	100.0	1043	6	ARU22178	ArU22178 Protein e	760	20	87.0	11	ADC44572	Adc44572 Endotheli
688	23	100.0	1070	7	ADC94089	Adc94089 E. faeciu	761	20	87.0	11	AAW23623	Aaw23623 Rat prola
689	23	100.0	1090	4	ABP98840	Abp98840 Human str	762	20	87.0	11	AAW23623	Aaw23623 Rat prola
690	23	100.0	1094	4	ABG28526	Abg28526 Novel hum	763	20	87.0	13	AAW23623	Aaw23623 Rat prola
691	23	100.0	1098	6	ABO07120	AbO07120 Novel hum	764	20	87.0	13	AAW23623	Aaw23623 Rat prola
692	23	100.0	1109	5	ABR91480	AbR91480 Herbicida	765	20	87.0	13	AAW23623	Aaw23623 Rat prola
693	23	100.0	1134	6	ABR53120	AbR53120 Protein s	766	20	87.0	15	AAW23623	Aaw23623 Rat prola
694	23	100.0	1152	6	ABM67058	AbM67058 Phototrab	767	20	87.0	15	AAW23623	Aaw23623 Rat prola
695	23	100.0	1166	6	ABU40581	AbU40581 Protein e	768	20	87.0	15	AAW23623	Aaw23623 Rat prola
696	23	100.0	1177	1	AAU70187	Aau70187 Plasmid p	769	20	87.0	19	AAW23623	Aaw23623 Rat prola
697	23	100.0	1180	4	ABM60588	AbM60588 Drosophil	770	20	87.0	20	AAW23623	Aaw23623 Rat prola
698	23	100.0	1184	7	ADD06553	AdD06553 Human Ckb	771	20	87.0	20	AAW23623	Aaw23623 Rat prola
699	23	100.0	1189	2	AAR08399	Aar08399 Human Ser	772	20	87.0	22	AAW23623	Aaw23623 Rat prola
700	23	100.0	1190	4	ABM60516	AbM60516 Drosophil	773	20	87.0	24	AAW23623	Aaw23623 Rat prola
701	23	100.0	1225	4	AAU18529	Aau18529 Human cyt	774	20	87.0	25	AAW23623	Aaw23623 Rat prola
702	23	100.0	1247	6	ABJ19352	AbJ19352 NOXK rela	775	20	87.0	25	AAW23623	Aaw23623 Rat prola
703	23	100.0	1248	4	ABM61571	AbM61571 Drosophil	776	20	87.0	25	AAW23623	Aaw23623 Rat prola
704	23	100.0	1257	2	AAV06427	Aav06427 Mouse cir	777	20	87.0	31	AAW23623	Aaw23623 Rat prola
705	23	100.0	1273	4	AAU41011	Aau41011 Human pol	778	20	87.0	31	AAW23623	Aaw23623 Rat prola
706	23	100.0	1279	4	ABG83047	AbG83047 S. epider	779	20	87.0	31	AAW23623	Aaw23623 Rat prola
707	23	100.0	1280	6	ABU00615	AbU00615 S. pneumo	780	20	87.0	31	AAW23623	Aaw23623 Rat prola
708	23	100.0	1327	5	ABP97286	Abp97286 Novel hum	781	20	87.0	31	AAW23623	Aaw23623 Rat prola
709	23	100.0	1381	2	AAR08032	Aar08032 Human Ser	782	20	87.0	31	AAW23623	Aaw23623 Rat prola
710	23	100.0	1443	6	ABG74688	AbG74688 Human CGD	783	20	87.0	31	AAW23623	Aaw23623 Rat prola
711	23	100.0	1493	4	AAU39225	Aau39225 Human pol	784	20	87.0	31	AAW23623	Aaw23623 Rat prola
712	23	100.0	1526	4	ABM63939	AbM63939 Drosophil	785	20	87.0	31	AAW23623	Aaw23623 Rat prola
713	23	100.0	1551	4	ABM64459	AbM64459 Drosophil	786	20	87.0	31	AAW23623	Aaw23623 Rat prola
714	23	100.0	1565	4	ABG18593	AbG18593 Novel hum	787	20	87.0	31	AAW23623	Aaw23623 Rat prola
715	23	100.0	1604	4	AAU47327	Aau47327 FCYR4. 8/	788	20	87.0	31	AAW23623	Aaw23623 Rat prola
716	23	100.0	1775	4	ABM64008	AbM64008 Drosophil	789	20	87.0	31	AAW23623	Aaw23623 Rat prola
717	23	100.0	1798	4	ABU71695	AbU71695 Drosophil	790	20	87.0	31	AAW23623	Aaw23623 Rat prola
718	23	100.0	1917	6	ABP99738	Abp99738 Polypepti	791	20	87.0	31	AAW23623	Aaw23623 Rat prola
719	23	100.0	1967	6	AAE35342	Aae35342 Human col	792	20	87.0	31	AAW23623	Aaw23623 Rat prola
720	23	100.0	1967	6	AAE35342	Aae35342 Human col	793	20	87.0	31	AAW23623	Aaw23623 Rat prola
721	23	100.0	2001	6	ABU70405	AbU70405 Human chr	794	20	87.0	31	AAW23623	Aaw23623 Rat prola
722	23	100.0	2051	6	AAO19619	Aao19619 Human nuc	795	20	87.0	31	AAW23623	Aaw23623 Rat prola
723	23	100.0	2061	4	ABM66938	AbM66938 Drosophil	796	20	87.0	31	AAW23623	Aaw23623 Rat prola
724	23	100.0	2061	4	ABM66938	AbM66938 Drosophil	797	20	87.0	31	AAW23623	Aaw23623 Rat prola
725	23	100.0	2215	5	ABM85015	AbM85015 Pain regu	798	20	87.0	31	AAW23623	Aaw23623 Rat prola
726	23	100.0	2215	5	ABM85015	AbM85015 Pain regu	799	20	87.0	31	AAW23623	Aaw23623 Rat prola
727	23	100.0	2228	7	ABR61599	AbR61599 Human gol	800	20	87.0	31	AAW23623	Aaw23623 Rat prola
728	23	100.0	2230	6	ABU07445	AbU07445 Protein d	801	20	87.0	31	AAW23623	Aaw23623 Rat prola
729	23	100.0	2230	6	ABU07445	AbU07445 Protein d	802	20	87.0	31	AAW23623	Aaw23623 Rat prola
730	23	100.0	2250	7	ABR61601	AbR61601 Human gol	803	20	87.0	31	AAW23623	Aaw23623 Rat prola
731	23	100.0	2252	7	ABR61602	AbR61602 Human gol	804	20	87.0	31	AAW23623	Aaw23623 Rat prola
732	23	100.0	2370	4	ABM60250	AbM60250 Drosophil	805	20	87.0	31	AAW23623	Aaw23623 Rat prola
733	23	100.0	2457	6	ABU21930	AbU21930 Protein e	806	20	87.0	31	AAW23623	Aaw23623 Rat prola
734	23	100.0	2559	2	AAU41012	Aau41012 Amino aci	807	20	87.0	31	AAW23623	Aaw23623 Rat prola
735	23	100.0	2559	2	AAU41012	Aau41012 Amino aci	808	20	87.0	31	AAW23623	Aaw23623 Rat prola
736	23	100.0	2670	4	ABM88126	AbM88126 Human IP3	809	20	87.0	31	AAW23623	Aaw23623 Rat prola
737	23	100.0	2670	4	ABM88126	AbM88126 Human IP3	810	20	87.0	31	AAW23623	Aaw23623 Rat prola
738	23	100.0	3079	2	AAU59926	Aau59926 GAP prote	811	20	87.0	31	AAW23623	Aaw23623 Rat prola
739	23	100.0	3084	2	AAU59926	Aau59926 GAP prote	812	20	87.0	31	AAW23623	Aaw23623 Rat prola
740	23	100.0	3084	2	AAU59926	Aau59926 GAP prote	813	20	87.0	31	AAW23623	Aaw23623 Rat prola
741	23	100.0	3111	4	ABM60327	AbM60327 Drosophil	814	20	87.0	31	AAW23623	Aaw23623 Rat prola
742	23	100.0	3269	6	ABP54436	Abp54436 Papaya le	815	20	87.0	31	AAW23623	Aaw23623 Rat prola
743	23	100.0	3542	4	ABM62142	AbM62142 P. falcip	816	20	87.0	31	AAW23623	Aaw23623 Rat prola
744	23	100.0	3673	6	ABM68688	AbM68688 Phototrab	817	20	87.0	31	AAW23623	Aaw23623 Rat prola
745	23	100.0	3692	6	ABU43311	AbU43311 Protein e	818	20	87.0	31	AAW23623	Aaw23623 Rat prola
746	23	100.0	3696	5	ABP40235	AbP40235 Staphyloc	819	20	87.0	31	AAW23623	Aaw23623 Rat prola
747	23	100.0	4820	4	ABM58592	AbM58592 Drosophil	820	20	87.0	31	AAW23623	Aaw23623 Rat prola
748	23	100.0	4861	5	AAU84280	Aau84280 Human end	821	20	87.0	31	AAW23623	Aaw23623 Rat prola
749	23	100.0	4861	5	AAU84280	Aau84280 Human end	822	20	87.0	31	AAW23623	Aaw23623 Rat prola
750	23	100.0	4861	5	AAU84280	Aau84280 Human end	823	20	87.0	31	AAW23623	Aaw23623 Rat prola
751	23	100.0	5373	4	AAU14697	Aau14697 Novel bon	824	20	87.0	31	AAW23623	Aaw23623 Rat prola
752	23	100.0	5447	4	AAU14697	Aau14697 Novel bon	825	20	87.0	31	AAW23623	Aaw23623 Rat prola
753	23	100.0	5447	4	AAU14697	Aau14697 Novel bon	826	20	87.0	31	AAW23623	Aaw23623 Rat prola
754	23	100.0	5447	4	AAU14697	Aau14697 Novel bon	827	20	87.0	31	AAW23623	Aaw23623 Rat prola
755	23	100.0	5447	4	AAU14697	Aau14697 Novel bon	828	20	87.0	31	AAW23623	Aaw23623 Rat prola

Abu02321 S. pneumo

829	20	87.0	59	4	AAU48607	AAU48607	Propionib	902	87.0	84	6	ABM63519	ABM63519	Propionib
830	20	87.0	59	6	ABM45126	ABM45126	Propionib	903	87.0	85	4	AAU67726	AAU67726	Propionib
831	20	87.0	60	4	AAU43739	AAU43739	Propionib	904	87.0	85	6	ABM64245	ABM64245	Propionib
832	20	87.0	60	5	ABP07135	ABP07135	Human ORF	905	87.0	86	2	AAW66350	AAW66350	Cathepsin
833	20	87.0	60	6	ABM40258	ABM40258	Propionib	906	87.0	86	4	AAU15688	AAU15688	Peptide #
834	20	87.0	62	4	AAU44216	AAU44216	Propionib	907	87.0	86	4	AAU28192	AAU28192	Peptide #
835	20	87.0	62	4	AAU50652	AAU50652	Propionib	908	87.0	86	4	ABM29511	ABM29511	Peptide #
836	20	87.0	62	4	AAU63496	AAU63496	Propionib	909	87.0	86	4	ABM20098	ABM20098	Protein #
837	20	87.0	62	6	ABM60015	ABM60015	Propionib	910	87.0	86	4	AAU67867	AAU67867	Human bon
838	20	87.0	62	6	ABM40735	ABM40735	Propionib	911	87.0	86	4	AAU55482	AAU55482	Human liv
839	20	87.0	62	6	ABM47171	ABM47171	Propionib	912	87.0	86	4	ABG49511	ABG49511	Human bra
840	20	87.0	63	4	AAU52464	AAU52464	Propionib	913	87.0	86	4	ABG49511	ABG49511	Human liv
841	20	87.0	63	6	ABM48983	ABM48983	Propionib	914	87.0	86	4	AAU03424	AAU03424	Peptide #
842	20	87.0	64	4	AAU44715	AAU44715	Propionib	915	87.0	86	5	ABG37414	ABG37414	Human pep
843	20	87.0	64	4	AAU44715	AAU44715	Propionib	916	87.0	86	6	ABM4696	ABM4696	Propionib
844	20	87.0	66	5	ABP04669	ABP04669	Human ORF	917	87.0	87	4	AAU60416	AAU60416	Human gen
845	20	87.0	67	4	AAU39252	AAU39252	Propionib	918	87.0	87	4	AAU57244	AAU57244	Human alb
846	20	87.0	67	6	ABM35771	ABM35771	Propionib	919	87.0	87	5	ABG63698	ABG63698	Human alb
847	20	87.0	68	4	AAU28336	AAU28336	Human dig	920	87.0	87	5	ABM56935	ABM56935	Propionib
848	20	87.0	68	4	AAU44715	AAU44715	Propionib	921	87.0	87	6	ABM33763	ABM33763	Propionib
849	20	87.0	68	5	ABP06151	ABP06151	Human ORF	922	87.0	87	6	ADA48000	ADA48000	Rice prot
850	20	87.0	68	6	ABM41234	ABM41234	Propionib	923	87.0	88	2	AAW88828	AAW88828	Polypepti
851	20	87.0	69	4	ABG30198	ABG30198	Novel hum	924	87.0	88	4	ABBS0777	ABBS0777	Human sec
852	20	87.0	70	4	AAU60967	AAU60967	Propionib	925	87.0	88	6	ABO45034	ABO45034	Novel hum
853	20	87.0	70	6	ABM57486	ABM57486	Propionib	926	87.0	88	7	ABO26514	ABO26514	Protein a
854	20	87.0	71	2	AAU60082	AAU60082	Human end	927	87.0	88	7	ABO26514	ABO26514	Protein a
855	20	87.0	71	3	AAU60993	AAU60993	Zea may	928	87.0	89	2	ABM62702	ABM62702	Propionib
856	20	87.0	71	4	AAU67693	AAU67693	Propionib	929	87.0	89	2	ABM62702	ABM62702	Propionib
857	20	87.0	71	4	AAU44404	AAU44404	Propionib	930	87.0	89	4	ABM44594	ABM44594	Murine CP
858	20	87.0	71	6	ABG15549	ABG15549	Novel hum	931	87.0	89	4	AAU45094	AAU45094	Murine wou
859	20	87.0	71	6	ABM40923	ABM40923	Propionib	932	87.0	89	4	AAU41378	AAU41378	Propionib
860	20	87.0	73	3	AAU64212	AAU64212	Propionib	933	87.0	89	6	ABM82709	ABM82709	Murine MR
861	20	87.0	73	3	AAU60534	AAU60534	Human sec	934	87.0	89	6	ABM37897	ABM37897	Propionib
862	20	87.0	73	4	AAU61284	AAU61284	Propionib	935	87.0	90	4	AAU55156	AAU55156	Propionib
863	20	87.0	73	4	AAU58953	AAU58953	Propionib	936	87.0	90	4	AAU55156	AAU55156	Propionib
864	20	87.0	73	6	ABM57803	ABM57803	Propionib	937	87.0	90	6	ABM51675	ABM51675	Propionib
865	20	87.0	73	7	ABM55472	ABM55472	Propionib	938	87.0	92	4	AAU66183	AAU66183	Propionib
866	20	87.0	74	4	ABM16610	ABM16610	Human ner	939	87.0	92	5	ABM78893	ABM78893	Propionib
867	20	87.0	74	4	ABM16610	ABM16610	Human ner	940	87.0	92	6	ABM62702	ABM62702	Propionib
868	20	87.0	74	6	ABM35846	ABM35846	Propionib	941	87.0	92	6	ABM62702	ABM62702	Propionib
869	20	87.0	75	4	AAU61506	AAU61506	Propionib	942	87.0	93	7	ADC96253	ADC96253	E. faeciu
870	20	87.0	75	4	AAU65615	AAU65615	Propionib	943	87.0	93	7	ADC96253	ADC96253	E. faeciu
871	20	87.0	75	6	ABM62134	ABM62134	Propionib	944	87.0	94	5	ABM78893	ABM78893	Propionib
872	20	87.0	75	6	ABM58025	ABM58025	Propionib	945	87.0	94	5	ABM78893	ABM78893	Propionib
873	20	87.0	75	6	ADA22879	ADA22879	Propionib	946	87.0	94	5	ABM78893	ABM78893	Propionib
874	20	87.0	77	4	AAU49429	AAU49429	Propionib	947	87.0	96	2	ABP76895	ABP76895	N. gonorr
875	20	87.0	77	4	AAU59016	AAU59016	Propionib	948	87.0	98	2	AAU14540	AAU14540	Streptoco
876	20	87.0	77	4	AAU45424	AAU45424	Propionib	949	87.0	98	3	AAU00958	AAU00958	Human sec
877	20	87.0	77	4	AAU64197	AAU64197	Propionib	950	87.0	98	4	AAU47157	AAU47157	Propionib
878	20	87.0	77	6	ABM45948	ABM45948	Propionib	951	87.0	98	5	ABM43676	ABM43676	Propionib
879	20	87.0	77	6	ABM55535	ABM55535	Propionib	952	87.0	99	5	ABE33343	ABE33343	Propionib
880	20	87.0	77	6	ABM60716	ABM60716	Propionib	953	87.0	101	6	ABP78296	ABP78296	N. gonorr
881	20	87.0	77	6	ABM41943	ABM41943	Propionib	954	87.0	102	4	AAU48893	AAU48893	Human imm
882	20	87.0	77	6	ADA22882	ADA22882	Propionib	955	87.0	103	3	AAU41058	AAU41058	Human ORF
883	20	87.0	78	4	AAU41878	AAU41878	Propionib	956	87.0	103	3	AAU54132	AAU54132	Arabidops
884	20	87.0	78	6	ABM38337	ABM38337	Propionib	957	87.0	103	3	AAU54132	AAU54132	Arabidops
885	20	87.0	79	2	AAU63593	AAU63593	MAP-Kinas	958	87.0	103	4	AAU11211	AAU11211	Human pol
886	20	87.0	80	2	AAU11722	AAU11722	Human 5'	959	87.0	103	4	AAU52830	AAU52830	Propionib
887	20	87.0	80	4	AAU00953	AAU00953	Human pol	960	87.0	103	6	ABM49349	ABM49349	Propionib
888	20	87.0	80	4	AAU39895	AAU39895	Propionib	961	87.0	104	4	ABM68492	ABM68492	Amino aci
889	20	87.0	80	4	AAU44873	AAU44873	Propionib	962	87.0	104	4	ABM67789	ABM67789	Drosophi
890	20	87.0	80	6	ABM36414	ABM36414	Propionib	963	87.0	104	5	ABP06719	ABP06719	Human ORF
891	20	87.0	80	6	ABM41392	ABM41392	Propionib	964	87.0	104	5	ABP06719	ABP06719	Human ORF
892	20	87.0	82	4	AAU66482	AAU66482	Propionib	965	87.0	105	4	AAU58723	AAU58723	Propionib
893	20	87.0	82	6	ABM63001	ABM63001	Propionib	966	87.0	105	6	ABM55242	ABM55242	Propionib
894	20	87.0	83	4	AAU53304	AAU53304	Propionib	967	87.0	106	4	AAU46300	AAU46300	Propionib
895	20	87.0	83	5	ABP04418	ABP04418	Human ORF	968	87.0	106	5	ABP10289	ABP10289	Human ORF
896	20	87.0	83	6	ABM49823	ABM49823	Propionib	969	87.0	106	5	ABU05403	ABU05403	M. tuberc
897	20	87.0	84	4	AAU48564	AAU48564	Propionib	970	87.0	106	6	ABM42819	ABM42819	Propionib
898	20	87.0	84	4	AAU51507	AAU51507	Propionib	971	87.0	107	3	AAU54451	AAU54451	Zea may
899	20	87.0	84	4	AAU67000	AAU67000	Propionib	972	87.0	110	3	AAU07125	AAU07125	Arabidops
900	20	87.0	84	6	ABM45083	ABM45083	Propionib	973	87.0	110	4	AAU00499	AAU00499	Human pol
901	20	87.0	84	6	ABM48026	ABM48026	Propionib	974	87.0	110	5	ABP34331	ABP34331	Human ORF

975 20 87.0 111 3 AAG58334 Arabidops  
976 20 87.0 111 4 AAM85333 Human imm  
977 20 87.0 111 4 AAM61097 Propionib  
978 20 87.0 111 6 AAM57616 Propionib  
979 20 87.0 113 2 AAR15677 SYNTH-9  
980 20 87.0 113 4 AAO09601 Human pol  
981 20 87.0 116 2 AAW64552 Human sto  
982 20 87.0 116 2 AAW59877 Amino aci  
983 20 87.0 116 2 AAW71627 Human hea  
984 20 87.0 116 5 ABB07624 Wheat nic  
985 20 87.0 116 6 ADA20759 Corn phos  
986 20 87.0 120 3 AAY66754 Membrane-  
987 20 87.0 120 3 AAB24077 Human PRO  
988 20 87.0 120 4 AAB65277 Human PRO  
989 20 87.0 120 5 ABB69105 Human PRO  
990 20 87.0 120 5 AAU83640 Human PRO  
991 20 87.0 120 6 ABUS8092 Human PRO  
992 20 87.0 120 6 ABUS9170 Novel hum  
993 20 87.0 120 6 ABUS2682 Human sec  
994 20 87.0 120 6 ABUS0601 Human sec  
995 20 87.0 120 6 ABUS0787 Human PRO  
996 20 87.0 120 6 ABO33753 Novel hum  
997 20 87.0 120 6 ABUI3983 Human PRO  
998 20 87.0 120 6 ABUS2568 Novel hum  
999 20 87.0 120 6 ABUS9317 Human sec  
1000 20 87.0 120 8 ADD74799 Human PRO

# ALIGNMENTS

RESULT 1  
AAY90711 standard; peptide; 4 AA.

XX AAY90711;  
AC  
XX  
DT 14-AUG-2000 (first entry)  
DE Human albumin N-terminal metal binding site peptide SEQ ID NO:1.  
XX  
XX Human; albumin; metal binding site; detection; free radical damage;  
KW blood; Parkinson's disease; Alzheimer's disease; cataractogenesis;  
KW atherosclerosis; diabetes mellitus; ischaemia-reperfusion injury;  
KW toxicity.  
XX Homo sapiens.  
XX OS  
XX WO200020454-A1.  
XX  
XX PD 13-APR-2000.  
XX  
XX PF 01-OCT-1999; 99WO-US022746.  
XX  
XX PR 02-OCT-1998; 98US-00165961.  
XX PR 02-OCT-1998; 98US-0102962P.  
XX  
XX PA (DIAG-) DIAGNOSTIC MARKERS INC.  
XX  
XX PI Bar-Or D, Lau E;  
XX  
XX WPI; 2000-303746/26.  
XX  
XX Sensitive marker for detection of free radical damage comprising modified  
PT albumin, useful for detecting diseases associated with free radicals such  
PT as neurodegenerative diseases and cancers.  
XX  
XX Claim 15; Page 31; 40pp; English.  
XX  
XX The present invention describes a marker (I) for the detection of free  
CC radical damage, comprising albumin which is modified in a manner  
CC resulting in inhibition of metal binding capacity of the N-terminus. Also  
CC described are methods for detecting and quantifying (I). The methods are

CC useful for detecting diseases associated with free radicals including  
CC Parkinson's, Alzheimer's, cataractogenesis, atherosclerosis, diabetes  
CC mellitus, ischaemia-reperfusion injury and certain toxicities. (I) is  
CC useful as a biochemical tag, allowing for sensitive detection and  
CC measurement of the efficacy of clinical drugs and therapeutics which  
CC result in the generation of free radicals or which act to limit free  
CC radical damage. (I) is a marker for the existence and detection and/or  
CC measurement of free radical damage which is highly sensitive and present  
CC in a majority of human fluids and tissues. The present sequence  
CC represents the specifically claimed human albumin N-terminal metal  
CC binding site  
XX  
SQ Sequence 4 AA;  
Query Match 100.0%; Score 23; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DAHK 4  
Db 1 DAHK 4  
RESULT 2  
AAB74365  
ID AAB74365 standard; peptide; 4 AA.  
XX  
XX AC AAB74365;  
XX  
XX DT 02-JUL-2001 (first entry)  
XX  
XX DE Reactive oxygen species inhibitory peptide.  
XX ROS; reactive oxygen species; metal binding; ischemia; neurodegenerative.  
XX Synthetic.  
XX OS  
XX WO200125265-A1.  
XX  
XX PD 12-APR-2001.  
XX  
XX PF 29-SEP-2000; 2000WO-US026952.  
XX  
XX PR 01-OCT-1999; 99US-0157404P.  
XX PR 13-JUN-2000; 2000US-0211078P.  
XX  
XX PA (BARO/) BAR-OR D.  
XX PA (CORT/) CORTIS C G.  
XX PA (LAUE/) LAU E.  
XX PA (RAON/) RAO N K R.  
XX PA (WINK/) WINKLER J V.  
XX PA (CROO/) CROOK W M.  
XX  
XX PI Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;  
XX  
XX WPI; 2001-328322/34.  
XX  
XX Metal binding peptide compounds prevent damage by reactive oxygen species  
PT in animal organs and tissues, useful for reperfusion, transplantation and  
PT treating e.g. ischemia, neurological and cardiovascular diseases.  
XX  
XX Example 10; Page 43; 124pp; English.  
XX  
XX The present invention relates to metal binding peptides that prevent  
CC damage by reactive oxygen. The peptides may be used for reperfusion an  
CC ischemic tissue or organ with cerebral or cardiovascular ischemia, for  
CC treating neurological trauma and for neurodegenerative disease. The  
CC present sequence is a reactive oxygen species inhibitory peptide  
XX  
SQ Sequence 4 AA;  
Query Match 100.0%; Score 23; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 Db 1 DAHK 4

RESULT 3  
 AAB86898  
 ID AAB86898 standard; peptide; 4 AA.  
 AC AAB86898;  
 XX  
 DT 28-NOV-2001 (first entry)  
 XX  
 DE Transport molecule/ligand binding-associated peptide #44.  
 XX  
 KW Transport molecule; ligand; cancer treatment; autoimmune disease;  
 KW inflammation; infection.  
 XX  
 OS Synthetic.  
 XX  
 XX WO200168142-A1.  
 PN  
 XX 20-SEP-2001.  
 PD  
 XX  
 PF 13-MAR-2001; 2001WO-EP002833.  
 XX  
 PR 13-MAR-2000; 2000DE-01012120.  
 XX  
 PA (KTET-) KTB TUMORFORSCHUNGS GMBH.  
 XX  
 PI Kratz F;  
 XX  
 XX WPI; 2001-589998/66.  
 DR  
 XX  
 PT New ligand, comprising therapeutic or diagnostic agent bonded non-covalently with substance having high affinity to transport molecule.  
 PT  
 PT Disclosure; Page 41; 74pp; German.  
 PS  
 XX This invention describes novel ligands which bind to transport molecules, comprising a therapeutic and/or diagnostic agent (A) non-covalently bonded via a linkage cleavable in vivo depending on pH and/or enzymatically with a substance (B) having an association constant KA to a transport molecule of above  $10^3 \text{ M}^{-1}$ , is new. The medicaments are especially useful for the treatment of cancers, autoimmune diseases, acute and chronic inflammation and infections caused by viruses or microorganisms. The diagnostic kits are useful for the detection of these illnesses and for the detection of the transport molecule and/or its distribution in vivo. The ligands have excellent solubility in the medium at the site of action and are easy and inexpensive to convert into adducts, as the interaction with the transport material is physical.  
 CC AAB86843-AAB86920 represent peptides used to illustrate the method of the invention  
 CC  
 XX Sequence 4 AA;  
 SQ

Query Match 100.0%; Score 23; DB 4; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 Db 1 DAHK 4

RESULT 4  
 AAEL14799  
 ID AAEL14799 standard; peptide; 4 AA.  
 XX  
 AC AAEL14799;  
 XX

DT 24-FEB-2003 (first entry)  
 XX  
 DE Human serum albumin N-terminal metal binding peptide.  
 XX  
 KW Reactive oxygen species; ROS; metal-binding peptide; angiogenesis; embryo implantation; endometriosis; tumour; hypertrophy; psoriasis; connective tissue disorder; ocular angiogenic disease; polyposis; cardiovascular disease; cerebral vascular disease; immune disorder; sepsis; obesity; acidosis; arthritis; asthma; autoimmune disease; cancer; cystic fibrosis; diabetes; hepatitis C; infertility; inflammation; inflammatory bowel disease; neurological disease; multiple sclerosis; pancreatitis; human; serum albumin.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO200264620-A2.  
 PN  
 XX 22-AUG-2002.  
 PD  
 XX  
 PF 13-FEB-2002; 2002WO-US004275.  
 XX  
 XX 13-FEB-2001; 2001US-0268558P.  
 PR 22-MAR-2001; 2001US-00816679.  
 PR 04-APR-2001; 2001US-0281648P.  
 PR 11-APR-2001; 2001US-0283507P.  
 XX  
 XX (DMTB-) DMI BIOSCIENCES INC.  
 PA  
 XX Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;  
 PI WPI; 2002-691590/74.  
 XX  
 DR  
 XX  
 PT New method for the inhibition of angiogenesis and the treatment of angiogenic disease, sepsis, and a disease involving acidosis, comprises the administration of a specified peptide or its salt.  
 PT  
 PT  
 XX  
 PS Example 1; Page 41; 129pp; English.  
 XX  
 CC The invention relates to a method for reducing molecular, cellular and tissue damage done by reactive oxygen species (ROS) and also reducing concentration of a metal ion in an animal using specific metal-binding peptides and their derivatives that bind metal ions. The compounds of the invention are useful for inhibiting angiogenesis (including required for embryo implantation e.g. in endometriosis), and for treating angiogenic diseases, such as tumour (preferably a benign tumour), tumour metastasis, hypertrophy, connective tissue disorder, psoriasis, ocular angiogenic disease, cardiovascular disease, cerebral vascular disease, polyposis, obesity, immune disorder, sepsis, and a disease or condition involving acidosis. The compounds are also useful in the treatment of ARDS, aging, AIDS, arteriosclerosis (hypertension, senility and impotence), arthritis, asthma, autoimmune diseases, cancer, chronic granulomatous disease, cirrhosis, colitis, Crohn's disease, cystic fibrosis, neurodegenerative diseases, diabetes (diabetic retinopathy, renal disease, impotence and peripheral vascular disease), eye diseases, emphysema, head and traumatic brain injury, hepatitis C, infertility, inflammation, inflammatory bowel disease, metastasis, ischaemia, neoplastic diseases, neurological diseases, multiple sclerosis, pancreatitis, peripheral vascular disease, prion disease, pulmonary embolism, reperfusion, scleroderma, sepsis, shock, tissue damage, toxic reactions (e.g. poisoning (herbicide, transition metal, carbon monoxide, and antibiotic toxicity). The present sequence is human serum albumin N-terminal peptide that binds Cu(II) and Ni(II) metals. The peptide and its derivatives are used in the invention

Query Match 100.0%; Score 23; DB 5; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 Db 1 DAHK 4

RESULT 5  
ABR39034  
ID ABR39034 standard; peptide; 4 AA.  
XX  
AC ABR39034;  
XX  
DT 10-MAY-2003 (first entry)  
XX  
DE Acylated polypeptide N-terminal extension peptide SEQ ID NO:35.  
XX  
XX Acylated, N-terminal extension.  
XX  
XX Synthetic.  
XX  
PN WO2003010186-A2.  
XX  
PD 06-FEB-2003.  
XX  
PF 18-JUL-2002; 2002WO-DK000502.  
XX  
PR 24-JUL-2001; 2001DK-00001141.  
XX  
PA (NOVO ) NOVO NORDISK AS.  
XX  
PI Diers I, Balschmidt P, Markussen J, Jonassen I, Egel-Mitani M;  
PI Kjeldsen TB;  
XX  
DR WPI; 2003-268032/26.  
XX  
XX Making polypeptides having at least one lysine residue in transformed  
PT host cells by expressing a precursor molecule of the desired polypeptide  
PT which is to be acylated and subsequently cleaved.  
XX  
XX Claim 31; Page 24; 42pp; English.  
XX  
CC The present invention describes making a polypeptide with at least one  
CC lysine residue being acylated in its epsilon-amino group, comprising  
CC culturing a host cell with a polynucleotide encoding and expressing a  
CC precursor molecule, separating the precursor from the culture broth,  
CC preferentially acylating the epsilon-amino group in the desired  
CC polypeptide, removing the N-terminal extension from the acylated  
CC precursor by enzymatic cleavage and isolating the acylated polypeptide.  
CC The precursor molecule comprises the desired polypeptide and an N-  
CC terminal extension cleavable from the desired polypeptide at a lysine  
CC cleavage site. The methods and compositions of the present invention are  
CC useful for the production of polypeptides in transformed host cells by  
CC expressing a precursor molecule of the desired polypeptide which is to be  
CC acylated and subsequently cleaved at a Lys cleavage site in a subsequent  
CC in vitro step. The present sequence represents a specifically claimed N-  
CC terminal extension peptide from the present invention  
XX  
SQ Sequence 4 AA;  
  
Query Match 100.0%; Score 23; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DAHK 4  
DB 1 DAHK 4  
  
RESULT 6  
ABP98620  
ID ABP98620 standard; peptide; 4 AA.  
XX  
AC ABP98620;  
XX  
DT 13-JUN-2003 (first entry)  
XX  
DE Cu-chelator peptide #1 for inhibiting copper-inactivation of APC.  
XX

KW anticoagulant; thrombolytic; antiinflammatory; antibacterial; antiulcer;  
KW immunosuppressive; antiasthmatic; antiparkinsonian; neuroleptic; asthma;  
KW antidepressant; antimanic; nootropic; dermatological; hypotensive;  
KW antiarteriosclerotic; antiallergic; activated protein C; APC; DVT;  
KW sepsis; coagulation disorder; inflammation; septic shock; hypertension;  
KW deep vein thrombosis; Parkinson's disease; schizophrenia; ulcer;  
KW manic depression; Huntington's disease; atherosclerosis; allergy.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1..4  
FT /note= "optionally D-form residues"  
XX  
PN WO2003007686-A2.  
XX  
PD 30-JAN-2003.  
XX  
PF 19-JUL-2002; 2002WO-US022951.  
XX  
PR 19-JUL-2001; 2001US-0307005P.  
PR 28-DEC-2001; 2001US-0344514P.  
XX  
PA (DMIB-) DMI BIOSCIENCES INC.  
XX  
XX Bar-Or D, Yukl RL;  
XX WPI; 2003-278307/27.  
XX  
XX Method for using active protein C (APC) comprising a copper chelator and  
PT protein C or protein C activator, useful for the treatment of coagulation  
PT disorders, inflammation, septic shock and deep vein thrombosis.  
XX  
XX Disclosure; Page 12; 68pp; English.  
XX  
XX The invention relates to a method of treating diseases treatable with  
CC activated protein C (APC) by inhibiting the inactivation of APC by copper  
CC (Cu) ions. The method includes the administration of a copper chelator,  
CC and APC, protein C (and/or an agent that increases synthesis of protein  
CC C), and/or an activator of protein C. Peptides ABP98620-ABP98624 are  
CC examples of Cu chelators that can be used in the method of the invention.  
CC The peptides are based on the sequence of high-affinity N-terminal Cu-  
CC binding motifs from serum albumins. The method can be used for treating  
CC animals in need of APC due to suffering from an acquired hypercoagulable  
CC state or an acquired protein C deficiency, sepsis, or a condition  
CC associated with intravascular coagulation. The method can also be used  
CC for preventing and treating coagulation disorders, inflammation, septic  
CC shock, deep vein thrombosis, asthma, Parkinson's disease, schizophrenia,  
CC manic depression, Huntington's disease, SLE, atherosclerosis,  
CC hypertension, ulcers and allergies  
XX  
SQ Sequence 4 AA;  
  
Query Match 100.0%; Score 23; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DAHK 4  
DB 1 DAHK 4  
  
RESULT 7  
ABP98473  
ID ABP98473 standard; peptide; 4 AA.  
XX  
AC ABP98473;  
XX  
DT 11-AUG-2003 (first entry)  
XX  
DE Amino acid sequence of a peptide.  
XX  
XX Mass spectrometry; spectrometer; mass filtering ion; charged ion;  
KW

Diers I, Balschmidt P, Markussen J, Jonassen I, Egel-Mitani M; Kjeldsen TB;  
WPI; 2003-268032/26.  
Making polypeptides having at least one lysine residue in transformed host cells by expressing a precursor molecule of the desired polypeptide which is to be acylated and subsequently cleaved.  
Claim 17; Page 22; 42pp; English.  
The present invention describes making a polypeptide with at least one lysine residue being acylated in its epsilon-amino group, comprising a culturing a host cell with a polynucleotide encoding and expressing a precursor molecule, separating the precursor from the culture broth, preferentially acylating the epsilon-amino group in the desired polypeptide, removing the N-terminal extension from the acylated precursor by enzymatic cleavage and isolating the acylated polypeptide. The precursor molecule comprises the desired polypeptide and an N-terminal extension cleavable from the desired polypeptide at a lysine cleavage site. The methods and compositions of the present invention are useful for the production of polypeptides in transformed host cells by expressing a precursor molecule of the desired polypeptide which is to be acylated and subsequently cleaved at a Lys cleavage site in a subsequent in vitro step. The present sequence represents a specifically claimed N-terminal extension peptide from the present invention  
Sequence 5 AA;  
Query Match 100.0%; Score 23; DB 6; Length 5;  
Best Local Similarity 100.0%; Pred. NO. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
QY 1 DAHK 4  
DB 2 DAHK 5  
RESULT 9  
AAW23611  
ID AAW23611 standard; peptide; 6 AA.  
XX AAW23611;  
XX AC  
XX AC  
XX AC  
DT 11-FEB-1998 (first entry)  
XX  
DE Prolactin antagonist (SI177A substituted C-terminal fragment).  
XX  
KW Prolactin antagonist; phosphorylation; hyperprolactinaemia; prolactinoma; prostate cancer; tumour; T-lymphoma; infertility; lactation; miscarriage; ovulation; antibody; therapy; rat.  
XX  
OS Rattus sp.  
OS Synthetic.  
XX  
XX WO9727865-A1.  
XX  
XX  
PD 07-AUG-1997.  
XX  
XX  
XX 30-JAN-1997; 97WO-US001435.  
XX  
XX 31-JAN-1996; 96US-00594809.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
PA  
XX Walker AM;  
XX  
XX WPI; 1997-402308/37.  
XX  
XX Substituted prolactin peptide(s) and proteins having an amino acid substitution for serine in the C-terminal - useful as prolactin antagonists, e.g. for treating prolactin dependent cancers.  
XX  
XX

PS Claim 4; Page 11; 158pp; English.

XX This peptide comprises a rat prolactin C-terminal fragment (amino acid residues 175-180) substituted at position 177 (serine in the native sequence) by alanine. It has prolactin antagonist activity, antagonising the stimulation of T lymphoma cell growth in the presence of non-phosphorylated prolactin. A method is claimed for preparation of recombinant prolactin substitution peptides (see AAT74327-32). The products (see AAW23607-19) can be used for the treatment of prolactin dependent cancers and can inhibit T-lymphoma cell proliferation. They are also useful for treatment of prolactinoma, infertility related to abnormal prolactin regulation, some forms of prostatic cancer, miscarriage and ovulation irregularities, as well as in assays to measure levels of non-phosphorylated and phosphorylated prolactin as an indicator of reproductive pathologies and presence or status of a prolactin-dependent tumour, and to raise polyclonal and monoclonal antibodies

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 23; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
|||||  
Db 2 DAHK 5

RESULT 10  
AAW23634  
ID AAW23634 standard; peptide; 6 AA.

AC AAW23634;

XX 11-FEB-1998 (first entry)

DE Human prolactin peptide (aal77-182, SI79A substituted).

KW Prolactin antagonist; phosphorylation; hyperprolactinaemia; prolactinoma;  
KW prostate cancer; tumour; T-lymphoma; infertility; lactation; therapy;  
KW human.

OS Homo sapiens.

OS Synthetic.

XX WO9727865-A1.

XX 07-AUG-1997.

XX 30-JAN-1997; 97WO-US001435.

XX 31-JAN-1996; 96US-00594809.

XX (REGC ) UNIV CALIFORNIA.

XX Walker AM;

XX WPI; 1997-402308/37.

XX Substituted prolactin peptide(s) and proteins having an amino acid substitution for serine in the C-terminal - useful as prolactin antagonists, e.g. for treating prolactin dependent cancers.

PS Disclosure; Page 14; 158pp; English.

XX This peptide comprises a human prolactin C-terminal fragment (amino acid residues 177-182) substituted at position 179 (serine in the native sequence) by alanine. Claimed substituted prolactin peptides and proteins (see AAW23607-19) have antagonistic activity with wild-type prolactin. They comprise substitution and monophosphorylated C-terminal fragments of prolactin containing a substituted serine residue (177 for rat, 179 for human). A method is claimed for preparation of recombinant prolactin substitution peptides (see AAT74327-32). The products can be used for the

CC treatment prolactin dependent cancers and can inhibit T-lymphoma cell proliferation. They are also useful for the treatment of prolactinoma, CC infertility related to abnormal prolactin regulation, some forms of CC prostatic cancer, ovulation irregularities and miscarriage, as well as in CC assays to measure levels of non-phosphorylated and phosphorylated CC prolactin as an indicator of reproductive pathologies and presence or CC status of a prolactin-dependent tumour, and to raise polyclonal and CC monoclonal antibodies

XX SQ Sequence 6 AA;

Query Match 100.0%; Score 23; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
|||||  
Db 2 DAHK 5

RESULT 11  
ABR39046  
ID ABR39046 standard; peptide; 7 AA.

XX ABR39046;

XX 10-MAY-2003 (first entry)

DE Acylated polypeptide N-terminal extension peptide SEQ ID NO:47.

XX Acylated; N-terminal extension.

XX Synthetic.

XX WO2003010186-A2.

XX 06-FEB-2003.

XX 18-JUL-2002; 2002WO-DK000502.

XX 24-JUL-2003; 2001DK-00001141.

XX (NOVO ) NOVO NORDISK AS.

XX Diers I, Balschmidt P, Markussen J, Jonassen I, Egel-Mitani M;  
XX Kjeldsen TB;

XX WPI; 2003-268032/26.

XX Making polypeptides having at least one lysine residue in transformed host cells by expressing a precursor molecule of the desired polypeptide which is to be acylated and subsequently cleaved.

PS Claim 17; Page 22; 42pp; English.

XX The present invention describes making a polypeptide with at least one lysine residue being acylated in its epsilon-amino group, comprising culturing a host cell with a polynucleotide encoding and expressing a precursor molecule, separating the precursor from the culture broth, preferentially acylating the epsilon-amino group in the desired polypeptide, removing the N-terminal extension from the acylated precursor by enzymatic cleavage and isolating the acylated polypeptide. The precursor molecule comprises the desired polypeptide and an N-terminal extension cleavable from the desired polypeptide at a lysine cleavage site. The methods and compositions of the present invention are useful for the production of polypeptides in transformed host cells by expressing a precursor molecule of the desired polypeptide which is to be acylated and subsequently cleaved at a lys cleavage site in a subsequent in vitro step. The present sequence represents a specifically claimed N-terminal extension peptide from the present invention

XX SQ Sequence 7 AA;



Query Match 100.0%; Score 23; DB 6; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;

QY 1 DAHK 4  
 DB 4 DAHK 7

RESULT 12  
 AAY90712  
 ID AAY90712 standard; peptide; 8 AA.

XX AC AAY90712;  
 XX DT 14-AUG-2000 (first entry)  
 XX DE Human albumin N-terminal octapeptide SEQ ID NO:2.

XX KW Human; albumin; metal binding site; detection; free radical damage;  
 KW blood; Parkinson's disease; Alzheimer's disease; cataractogenesis;  
 KW atherosclerosis; diabetes mellitus; ischaemia-reperfusion injury;  
 KW toxicity.

XX OS Homo sapiens.  
 XX FN WO200020454-A1.

XX PD 13-APR-2000.

XX PF 01-OCT-1999; 99WO-US022746.

XX PR 02-OCT-1998; 98US-00165961.

XX PR 02-OCT-1998; 98US-01029622.

XX PA (DIAG-) DIAGNOSTIC MARKERS INC.

XX PI Bar-Or D, Lau E;

XX DR WPI; 2000-303746/26.

XX PT Sensitive marker for detection of free radical damage comprising modified  
 PT albumin, useful for detecting diseases associated with free radicals such  
 PT as neurodegenerative diseases and cancers.

XX PS Example 1; Page 16; 40pp; English.

XX CC The present invention describes a marker (I) for the detection of free  
 CC radical damage, comprising albumin which is modified in a manner  
 CC resulting in inhibition of metal binding capacity of the N-terminus. Also  
 CC described are methods for detecting and quantifying (I). The methods are  
 CC useful for detecting diseases associated with free radicals including  
 CC Parkinson's, Alzheimer's, cataractogenesis, atherosclerosis, diabetes  
 CC mellitus, ischaemia-reperfusion injury and certain toxicities. (I) is  
 CC useful as a biochemical tag, allowing for sensitive detection and  
 CC measurement of the efficacy of clinical drugs and therapeutics which  
 CC result in the generation of free radicals or which act to limit free  
 CC radical damage. (I) is a marker for the existence and detection and/or  
 CC measurement of free radical damage which is highly sensitive and present  
 CC in a majority of human fluids and tissues. The present sequence  
 CC represents the human albumin N-terminal octapeptide which is used in  
 CC examples from the present invention to measure cobalt binding

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 DB 1 DAHK 4

RESULT 13  
 ABG70867  
 ID ABG70867 standard; peptide; 8 AA.

XX AC ABG70867;

XX DT 28-NOV-2002 (first entry)

XX DE Fluorescent binding peptide for determination of albumin in urine.

XX KW Analyte concentration; polarised light; binding ligand; blood test;  
 KW blood cell lysis; albumin; urine.

XX OS Homo sapiens.

XX FN WO200244721-A1.

XX PD 06-JUN-2002.

XX PF 30-NOV-2001; 2001WO-NO000480.

XX PR 01-DEC-2000; 2000NO-00006130.

XX PA (SUND/) SUNDREHAGEN E.

XX PI Sundrehagen E;

XX DR WPI; 2002-691469/74.

XX PT Determination of concentration of at least one analyte in a test sample  
 PT involves mixing the sample with a single reagent, irradiating the mixture  
 PT and calculating the concentration of the analyte.

XX PS Example 10; Page 43; 78pp; English.

XX CC The invention relates to the determination of concentration of at least  
 CC one analyte in a test sample or an aliquot of a test sample of a complex  
 CC biological fluid involves: (i) mixing the sample or aliquot of the sample  
 CC with one single reagent such as a solid, solution or premixed solution to  
 CC form a mixture (ii) irradiating the mixture with polarised light which  
 CC permits the excitation of the fluorescent molecules (iii) measuring the  
 CC polarisation of the emitted light, and (iv) calculating the  
 CC concentration(s) of the analyte(s). The reagent is provided in one single  
 CC container or compartment of a container and no other reagent is added  
 CC during the performance of the method. The reagent further comprises at  
 CC least one type of binding molecule with specific affinity for at least  
 CC one of the analytes and either fluorescent moieties covalently linked to  
 CC the binding molecules or fluorescent analogues, fluorescent fragments or  
 CC fluorescent derivatives of the analyte(s). The method is used for the  
 CC determination of concentration of at least one analyte in a test sample  
 CC or an aliquot of a test sample of a complex biological fluid.

XX CC particularly for the determination of concentrations of clinically  
 CC related substances in samples of biological material from a living  
 CC organism e.g. plants, insects, birds and animals such as mammals (e.g.  
 CC primates or humans). The method involves use of stable, durable reagents;  
 CC is carried out in very few (preferably just one single container); does  
 CC not require any significant pipette work. The method can be carried out  
 CC on blood tests after or with simultaneous lysis of the blood cells. The  
 CC method is a sensitive specific measurement method. The method is carried  
 CC out at constant temperature by use of correction algorithms empirically  
 CC generated by temperature's influence on test solutions with known  
 CC concentration of the analyte. The present sequence is a fluorescent  
 CC peptide for determination of albumin in urine (it is the N-terminus of  
 CC human albumin) using the method of the invention

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4

Db ||||  
1 DAHK 4

RESULT 14  
AAE13134  
ID AAE13134 standard; peptide; 9 AA.  
XX  
AC AAE13134;  
XX  
DT 28-JAN-2002 (first entry)  
XX  
DE Human albumin (HA) peptide.  
XX  
KW Human; albumin; HA; fusion protein; therapeutic protein; vulnary;  
KW immune system disorder; transplant rejection; blood related disorder;  
KW myocardial infarction; hyperproliferative disorder; glomerulonephritis;  
KW childhood acute myeloid leukemia; cardiovascular disorder; arrhythmia;  
KW respiratory disorder; gene therapy; non-allergic rhinitis; noctropic;  
KW neurological disease; Alzheimer's disease; reproductive system disorder;  
KW endocrine disorder; pheochromocytoma; infectious disease; antiarrhythmic;  
KW measles; gastrointestinal disorder; irritable bowel syndrome; syphilis;  
KW wound healing; antiinflammatory; immunosuppressive; neuroprotective;  
KW cardiant; cytostatic; antileukaemic; antirheumatic; antimicrobial;  
KW renal disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200179443-A2.  
XX  
PD 25-OCT-2001.  
XX  
XX 12-APR-2001; 2001WO-US011924.  
XX  
PF 12-APR-2000; 2000US-0229358P.  
PR 23-APR-2000; 2000US-0199384P.  
PR 21-DEC-2000; 2000US-0256931P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Haseltine WA;  
XX  
XX WPI; 2001-616754/71.  
XX  
XX Albumin fusion proteins comprising a therapeutic protein and albumin,  
PT useful in the treating immune system disorders (e.g. transplant  
PT rejection), blood related disorders (e.g. myocardial infarction) and  
PT hyperproliferative disorders.  
XX  
XX Example 2; Page 232; 380pp; English.  
XX  
XX The invention relates to albumin fusion proteins comprising therapeutic  
CC protein and human albumin (HA). Therapeutic protein fused to albumin have  
CC an extended shelf-life. The albumin fusion proteins are useful in the  
CC treatment, prevention, diagnosis and/or detection of diseases, disorders  
CC such as immune system disorders (e.g. transplant rejection), blood  
CC related disorders (e.g. myocardial infarction), hyperproliferative  
CC disorders (e.g. childhood acute myeloid leukemia), renal disorders (e.g.  
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmias),  
CC respiratory disorders (e.g. non-allergic rhinitis), neurological diseases  
CC (e.g. Alzheimer's disease), endocrine disorders (e.g. pheochromocytoma),  
CC reproductive system disorders (e.g. syphilis), infectious diseases (e.g.  
CC measles), gastrointestinal disorders (e.g. irritable bowel syndrome) and  
CC wound healing. Nucleic acids encoding albumin fusion protein is used in  
CC gene therapy. The present sequence is human albumin (HA) peptide  
XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DAHK 4

Db ||||  
1 DAHK 4

RESULT 15  
ABR39047  
ID ABR39047 standard; peptide; 9 AA.  
XX  
AC ABR39047;  
XX  
DT 10-MAY-2003 (first entry)  
XX  
DE Acylated polypeptide N-terminal extension peptide SEQ ID NO:48.  
XX  
KW Acylated; N-terminal extension.  
XX  
OS Synthetic.  
XX  
PN WO2003010186-A2.  
XX  
PD 06-FEB-2003.  
XX  
PF 18-JUL-2002; 2002WO-DK000502.  
XX  
PR 24-JUL-2001; 2001DK-00001141.  
XX  
XX (NOVO ) NOVO NORDISK AS.  
XX  
XX Diers I, Balschmidt P, Markussen J, Jonassen I, Egel-Mitani M;  
XX Kjeldeen TB;  
XX  
XX WPI; 2003-268032/26.  
XX  
XX Making polypeptides having at least one lysine residue in transformed  
PT host cells by expressing a precursor molecule of the desired polypeptide  
PT which is to be acylated and subsequently cleaved.  
XX  
XX Claim 17; Page 22; 42pp; English.  
XX  
XX The present invention describes making a polypeptide with at least one  
CC lysine residue being acylated in its epsilon-amino group, comprising a  
CC culturing a host cell with a polynucleotide encoding and expressing a  
CC precursor molecule, separating the precursor from the culture broth,  
CC preferentially acylating the epsilon-amino group in the desired  
CC polypeptide, removing the N-terminal extension from the acylated  
CC precursor by enzymatic cleavage and isolating the acylated polypeptide.  
CC The precursor molecule comprises the desired polypeptide and an N-  
CC terminal extension cleavable from the desired polypeptide at a lysine  
CC cleavage site. The methods and compositions of the present invention are  
CC useful for the production of polypeptides in transformed host cells by  
CC expressing a precursor molecule of the desired polypeptide which is to be  
CC acylated and subsequently cleaved at a Lys cleavage site in a subsequent  
CC in vitro step. The present sequence represents a specifically claimed N-  
CC terminal extension peptide from the present invention  
XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 DAHK 4  
Db 6 DAHK 9

Search completed: September 9, 2004, 23:45:53  
Job time : 191 secs

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OM protein - protein search, using sw model

Run on: September 9, 2004, 23:41:38 ; Search time 39 Seconds

(without alignments)  
9.866 Million cell updates/sec

Title: US-10-076-071-1

Perfect score: 23

Sequence: 1 DAHK 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR\_78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	87	C81890	hypothetical prote
2	23	100.0	92	T44734	hypothetical prote
3	23	100.0	94	AH0375	hypothetical prote
4	23	100.0	100	G86805	transcription regu
5	23	100.0	102	E75528	hypothetical prote
6	23	100.0	104	G43258	phosphotransferase
7	23	100.0	109	T45101	H+-transporting tw
8	23	100.0	112	G97473	hypothetical prote
9	23	100.0	116	C82906	ribosome binding f
10	23	100.0	118	B90155	hypothetical prote
11	23	100.0	121	T36836	hypothetical prote
12	23	100.0	122	C70965	hypothetical prote
13	23	100.0	122	C75371	conserved hypothet
14	23	100.0	124	T06427	aminopeptidase - t
15	23	100.0	125	D81138	succinate dehydrog
16	23	100.0	136	T39439	hypothetical prote
17	23	100.0	140	H8FGRG	hemoglobin beta ch
18	23	100.0	149	A47054	ferric uptake regu
19	23	100.0	151	RGSHSP	regulatory protein
20	23	100.0	155	A82841	hypothetical prote
21	23	100.0	168	C33601	low calcium respon
22	23	100.0	168	C37314	regulatory protein
23	23	100.0	170	T11964	allophycocyanin be
24	23	100.0	175	T09249	late embryonic abu
25	23	100.0	175	PH0261	hypothetical 17.8K
26	23	100.0	179	AH3630	outer-membrane lip
27	23	100.0	187	E89961	conserved hypothet
28	23	100.0	191	A96765	hypothetical prote
29	23	100.0	196	A39223	superoxide dismuta

30	23	100.0	205	2	T18215	hypothetical prote
31	23	100.0	207	1	S31011	probable phosphoes
32	23	100.0	207	2	JS0718	yafE protein - Esc
33	23	100.0	209	2	E75600	butyrate-acetoacet
34	23	100.0	211	2	T23696	hypothetical prote
35	23	100.0	211	2	F84467	hypothetical prote
36	23	100.0	212	2	B83543	hypothetical prote
37	23	100.0	216	2	D98240	probable hydrolase
38	23	100.0	216	2	B97992	conserved hypothet
39	23	100.0	218	1	VHVUSS	nucleocapsid prote
40	23	100.0	222	2	F95029	transaldolase fami
41	23	100.0	223	2	E64205	deoxyribose-phosph
42	23	100.0	224	2	S02216	deoxyribose-phosph
43	23	100.0	226	2	F83307	probable hydrolase
44	23	100.0	229	2	B95287	probable hydrolase
45	23	100.0	229	2	AH3045	hydrolase [impor
46	23	100.0	230	2	JC2582	somatolactin - Sen
47	23	100.0	230	2	JC5418	somatolactin precu
48	23	100.0	230	2	T12872	hypothetical prote
49	23	100.0	231	2	A35793	somatolactin Jap
50	23	100.0	233	2	A23729	somatolactin precu
51	23	100.0	235	2	A49762	somatolactin precu
52	23	100.0	235	2	H82262	hypothetical prote
53	23	100.0	236	2	C75181	hypothetical prote
54	23	100.0	236	2	H71032	hypothetical prote
55	23	100.0	237	2	S73504	degV protein homol
56	23	100.0	238	1	S44444	protein disulfide-
57	23	100.0	239	2	A13013	tolQ Protein limpo
58	23	100.0	245	2	S64105	probable membrane
59	23	100.0	256	2	F85505	unknown [imported]
60	23	100.0	256	2	F90654	probable biotin sy
61	23	100.0	262	2	F83498	hypothetical prote
62	23	100.0	263	2	TS2037	14-3-3 regulatory
63	23	100.0	271	2	D90924	probable lipoprote
64	23	100.0	271	2	H85772	probable lipoprote
65	23	100.0	271	2	A64923	hypothetical prote
66	23	100.0	277	2	I37552	hypothetical prote
67	23	100.0	280	2	JE0217	28k surface antige
68	23	100.0	283	2	S73524	probable lipoprote
69	23	100.0	285	2	F71076	hypothetical prote
70	23	100.0	285	2	F98270	tolQ protein limpo
71	23	100.0	286	2	F82881	hypothetical prote
72	23	100.0	289	2	AH0112	probable membrane
73	23	100.0	290	2	T21198	hypothetical prote
74	23	100.0	292	2	A64073	D-ribose-binding p
75	23	100.0	298	1	TVBY8	protein kinase (EC
76	23	100.0	299	2	C97102	hypothetical prote
77	23	100.0	305	2	S40927	hypothetical prote
78	23	100.0	310	2	T29355	hypothetical prote
79	23	100.0	319	2	A12125	hypothetical prote
80	23	100.0	324	2	AE3650	oxidoreductase (EC
81	23	100.0	326	2	T04344	peroxidase (EC 1.1
82	23	100.0	330	2	G95134	hypothetical prote
83	23	100.0	330	2	B98003	acetoin dehydrogen
84	23	100.0	331	2	F86835	hypothetical prote
85	23	100.0	333	1	A38094	D-lactate dehydrog
86	23	100.0	336	2	A82165	transcription regu
87	23	100.0	343	1	E70477	GTP-binding protei
88	23	100.0	343	2	AB0197	beta-N-acetylhexos
89	23	100.0	344	2	S38939	probable cathepsin
90	23	100.0	344	2	S59043	spilling factor SR
91	23	100.0	345	1	B46113	protein kinase (EC
92	23	100.0	345	2	S36959	dopamine receptor
93	23	100.0	347	2	E89788	hypothetical prote
94	23	100.0	347	2	T17645	hypothetical prote
95	23	100.0	350	2	A40459	nuclear phosphopro
96	23	100.0	351	2	T18066	hypothetical prote
97	23	100.0	351	2	T42421	hypothetical prote
98	23	100.0	358	2	D96722	hypothetical prote
99	23	100.0	360	2	C64628	lipid A disacchari
100	23	100.0	360	2	D71888	probable protein d
101	23	100.0	361	2	T00437	probable histidine
102	23	100.0	362	2	D72734	

103	23	100.0	366	2	B69949	phage-related prot	176	23	100.0	502	2	T36589	probable transmembr
104	23	100.0	368	2	T23315	hypothetical prote	177	23	100.0	502	2	A70985	probable polyketid
105	23	100.0	370	2	D87642	conserved hypotet	178	23	100.0	510	1	I64162	mnvN protein homol
106	23	100.0	372	2	T25717	hypothetical prote	179	23	100.0	510	2	G72464	hypothetical prote
107	23	100.0	374	2	A37282	52K active chromat	180	23	100.0	518	2	B83439	hypothetical prote
108	23	100.0	379	2	T04645	hypothetical prote	181	23	100.0	519	2	G97560	probable glucose-1
109	23	100.0	388	2	C69420	GTP-binding protei	182	23	100.0	522	2	AC3374	probable sugar kin
110	23	100.0	389	1	SAVL71	large surface anti	183	23	100.0	527	2	AE2380	type I restriction
111	23	100.0	389	2	F69594	8-amino-7-oxonon	184	23	100.0	527	2	T15258	hypothetical prote
112	23	100.0	390	2	JS0296	transposase - Stap	185	23	100.0	534	2	E84590	hypothetical prote
113	23	100.0	391	2	C87615	acyltransferase, p	186	23	100.0	535	2	S40461	t-complex-type mol
114	23	100.0	412	2	A86225	protein T12M4.7 [i	187	23	100.0	540	2	T26445	hypothetical prote
115	23	100.0	414	2	G69536	group II decarboxy	188	23	100.0	545	2	AB0290	probable membrane
116	23	100.0	420	2	S19707	site-specific DNA-	189	23	100.0	548	2	H82234	probable glutamate
117	23	100.0	420	2	D86617	CT857 hypothetical	190	23	100.0	549	2	H96944	arginine degradati
118	23	100.0	420	2	S36444	hygromycin phospho	191	23	100.0	550	2	AB3136	MFS permease [impo
119	23	100.0	420	2	E72006	probable im protei	192	23	100.0	552	2	B98152	hypothetical prote
120	23	100.0	421	1	HQDVIV	cytochrome-c3 hydr	193	23	100.0	558	2	T50742	protoporphyrin IX
121	23	100.0	422	2	G81532	Na+/H+ antiporter,	194	23	100.0	570	2	F70844	probable fusion pr
122	23	100.0	424	1	B49851	protochlorophyllid	195	23	100.0	595	2	T39228	beta-transducin -
123	23	100.0	425	2	T50355	hypothetical prote	196	23	100.0	601	2	H81282	probable translati
124	23	100.0	427	2	D81725	Na+/H+ antiporter,	197	23	100.0	601	2	T15260	hypothetical prote
125	23	100.0	428	1	CTBSBA	site-specific DNA-	198	23	100.0	605	2	S43568	beta transducin ho
126	23	100.0	428	2	D81255	histidinol dehydro	199	23	100.0	608	2	T51217	hypothetical prote
127	23	100.0	429	2	A33309	uterine milk prote	200	23	100.0	609	1	ABHUS	serum albumin prec
128	23	100.0	430	2	T37198	hypothetical prote	201	23	100.0	614	2	D87410	icold protein [impo
129	23	100.0	431	2	H82237	histidinol dehydro	202	23	100.0	620	2	S55086	probable membrane
130	23	100.0	436	2	T39299	probable proteosom	203	23	100.0	620	2	D86903	asparagine synthas
131	23	100.0	437	2	C97020	argininosuccinate	204	23	100.0	631	2	T33559	hypothetical prote
132	23	100.0	440	2	A70067	NDP-sugar dehydrog	205	23	100.0	668	2	B86831	hypothetical prote
133	23	100.0	441	2	H83763	6-phospho-beta-glu	206	23	100.0	686	2	T10548	hypothetical prote
134	23	100.0	441	2	E96666	hypothetical prote	207	23	100.0	695	2	A87494	topoisomerase IV,
135	23	100.0	442	1	DYXLD2	dopamine receptor	208	23	100.0	699	2	AC3594	DNA topoisomerase
136	23	100.0	442	2	T06669	hypothetical prote	209	23	100.0	702	2	H84189	lipote protein li
137	23	100.0	443	2	D86183	hypothetical prote	210	23	100.0	702	2	H90757	probable oxidoredu
138	23	100.0	445	2	B65221	probable amino aci	211	23	100.0	702	2	F85621	probable oxidoredu
139	23	100.0	445	2	A91266	probable amino aci	212	23	100.0	702	2	C64835	hypothetical prote
140	23	100.0	445	2	F86106	probable amino aci	213	23	100.0	703	2	T48600	kinase-like protei
141	23	100.0	445	2	AF1022	probable amino aci	214	23	100.0	717	2	F82613	VacB protein Xf198
142	23	100.0	446	2	D70597	probable signal pe	215	23	100.0	727	2	H69724	DNA topoisomerase
143	23	100.0	447	2	T34992	probable lipoprote	216	23	100.0	730	2	T05345	hypothetical prote
144	23	100.0	449	2	S16319	secretin receptor	217	23	100.0	731	2	S29870	DNA-binding protei
145	23	100.0	452	2	S27611	agglutination prot	218	23	100.0	743	2	S48917	probable regulator
146	23	100.0	456	2	S31125	26S proteasome reg	219	23	100.0	745	2	G84995	VacB protein [impo
147	23	100.0	457	2	AG2699	magnesium transpor	220	23	100.0	747	2	D96829	homeobox protein A
148	23	100.0	457	2	G97481	mg2+ transport pro	221	23	100.0	747	2	S71478	catalase (EC 1.11.
149	23	100.0	458	2	A75386	conserved hypotet	222	23	100.0	750	2	AB0708	catalase (EC 1.11.
150	23	100.0	459	2	AD1787	lysine decarboxyla	223	23	100.0	752	2	T09649	delta-1-pyrroline-
151	23	100.0	459	2	AE1411	lysine decarboxyla	224	23	100.0	752	2	F81203	maltose phosphoryl
152	23	100.0	464	2	C69356	conserved hypotet	225	23	100.0	752	2	C81781	probable maltose p
153	23	100.0	467	2	AE0735	probable bacteriop	226	23	100.0	753	2	A39129	catalase (EC 1.11.
154	23	100.0	467	2	AF0621	probable prophage	227	23	100.0	753	2	B85782	catalase, hydroler
155	23	100.0	469	1	A39358	histidinol dehydro	228	23	100.0	753	2	F90933	catalase, HPII [imp
156	23	100.0	470	1	WZBEA4	transcription acti	229	23	100.0	754	2	AP2849	methyl-accepting c
157	23	100.0	470	1	B42746	transcription acti	230	23	100.0	763	2	F96693	hypothetical prote
158	23	100.0	473	2	A38627	gamma-aminobutyric	231	23	100.0	765	2	T14564	inorganic diphosph
159	23	100.0	478	2	AC3386	glucose inhibited	232	23	100.0	766	2	S61424	inorganic diphosph
160	23	100.0	481	2	T37505	hypothetical prote	233	23	100.0	768	2	D97626	hypothetical prote
161	23	100.0	481	2	AG2781	glucose inhibited	234	23	100.0	770	2	T04792	hypothetical prote
162	23	100.0	483	2	H87492	YjeF family protei	235	23	100.0	783	2	AB3592	ribonuclease R [EC
163	23	100.0	484	2	F64554	guanosine pentapho	236	23	100.0	784	2	AG2736	exoribonuclease [i
164	23	100.0	484	2	F71954	guanosine-5'-triph	237	23	100.0	786	2	E97517	exoribonuclease RN
165	23	100.0	485	1	ANHU	angiotensin precu	238	23	100.0	786	2	G96940	hypothetical prote
166	23	100.0	485	2	D87478	coniferyl aldehyde	239	23	100.0	787	2	T05617	hypothetical prote
167	23	100.0	490	1	A43492	surface glycoprote	240	23	100.0	789	2	S28359	androgen-regulated
168	23	100.0	491	1	VXAPLV	surface glycoprote	241	23	100.0	791	2	G81109	ribonuclease II fa
169	23	100.0	493	2	C86565	oligopeptide perme	242	23	100.0	791	2	B81906	probable ribonucle
170	23	100.0	493	2	D72059	peptide ABC transp	243	23	100.0	791	2	C82940	hypothetical prote
171	23	100.0	494	2	JH0665	catechol oxidase (	244	23	100.0	799	2	G87378	phenylalanyl-trNA
172	23	100.0	494	2	A48133	pre-mRNA splicing	245	23	100.0	803	2	F90485	hypothetical prote
173	23	100.0	498	2	T39077	hypothetical prote	246	23	100.0	808	2	T16564	hypothetical prote
174	23	100.0	498	2	T10316	global transactiva	247	23	100.0	810	2	C70791	probable pona', pro
175	23	100.0	500	2	B81250	probable site-spec	248	23	100.0	812	2	AH1049	ribonuclease R (RN

probable transmembr  
probable polyketid  
mnvN protein homol  
hypothetical prote  
hypothetical prote  
probable glucose-1  
probable sugar kin  
type I restriction  
hypothetical prote  
hypothetical prote  
t-complex-type mol  
hypothetical prote  
probable membrane  
probable glutamate  
arginine degradati  
MFS permease [impo  
hypothetical prote  
protoporphyrin IX  
probable fusion pr  
beta-transducin -  
probable translati  
hypothetical prote  
beta transducin ho  
hypothetical prote  
icold protein [impo  
probable membrane  
asparagine synthas  
hypothetical prote  
hypothetical prote  
hypothetical prote  
topoisomerase IV,  
DNA topoisomerase  
lipote protein li  
probable oxidoredu  
probable oxidoredu  
hypothetical prote  
kinase-like protei  
VacB protein Xf198  
DNA topoisomerase  
hypothetical prote  
DNA-binding protei  
probable regulator  
vacB protein [impo  
homeobox protein A  
catalase (EC 1.11.  
catalase (EC 1.11.  
delta-1-pyrroline-  
maltose phosphoryl  
probable maltose p  
catalase (EC 1.11.  
catalase, hydroler  
catalase, HPII [imp  
methyl-accepting c  
hypothetical prote  
inorganic diphosph  
inorganic diphosph  
hypothetical prote  
hypothetical prote  
ribonuclease R [EC  
exoribonuclease [i  
exoribonuclease RN  
hypothetical prote  
hypothetical prote  
androgen-regulated  
ribonuclease II fa  
probable ribonucle  
hypothetical prote  
phenylalanyl-trNA  
hypothetical prote  
hypothetical prote  
probable pona', pro  
ribonuclease R (RN



395	20	87.0	170	2	T34588	hypothetical prote	468	20	87.0	229	2	A60972	prolactin precursor
396	20	87.0	172	2	T25066	hypothetical prote	469	20	87.0	229	2	JC4631	prolactin precursor
397	20	87.0	174	2	H83481	hypothetical prote	470	20	87.0	229	2	B37944	CAMP response elem
398	20	87.0	175	2	S18882	prolactin - Americ	471	20	87.0	229	2	A37944	CAMP response elem
399	20	87.0	176	2	A06684	bacteriophage host	472	20	87.0	229	2	A69971	conserved hypotet
400	20	87.0	177	2	T28106	prolactin, 20K - M	473	20	87.0	229	2	A89473	protein F52D2.2 [i
401	20	87.0	182	2	S75533	hydrogenase small	474	20	87.0	233	2	T20671	hypothetical prote
402	402	87.0	187	2	S06677	prolactin II - chu	475	20	87.0	234	2	G97225	diverged arginase
403	403	87.0	187	2	S02304	prolactin I - chum	476	20	87.0	235	2	S73536	uridylate kinase p
404	404	87.0	188	2	B28106	prolactin, 24K - M	477	20	87.0	235	2	C87687	acyltransferase fa
405	20	87.0	190	2	T26609	hypothetical prote	478	20	87.0	236	2	G69054	conserved hypotet
406	20	87.0	192	2	A10268	anthranilate synth	479	20	87.0	237	2	A45929	spectrin beta chai
407	20	87.0	192	2	S59537	heat shock transcr	480	20	87.0	237	2	S36343	opacity protein op
408	20	87.0	192	2	T06284	hypothetical prote	481	20	87.0	238	1	HHEF67	heat shock protein
409	20	87.0	196	2	D84178	50S ribosomal prot	482	20	87.0	238	2	D83847	two-component resp
410	20	87.0	196	2	B83226	aliphatic amidase	483	20	87.0	239	2	E86346	two-component resp
411	20	87.0	196	2	S03884	regulatory protein	484	20	87.0	240	1	G69691	hypothetical prote
412	20	87.0	198	1	A06620	prolactin - green	485	20	87.0	240	2	T14978	hypothetical prote
413	20	87.0	199	1	LC80	prolactin - horse	486	20	87.0	241	2	D89928	hypothetical prote
414	20	87.0	199	2	PN0128	prolactin - sei wh	487	20	87.0	242	2	A64155	hypothetical prote
415	20	87.0	199	2	JS0430	prolactin - elepha	488	20	87.0	242	2	T39231	probable lysophosp
416	20	87.0	199	2	S15131	prolactin - Arabia	489	20	87.0	242	2	AD2982	transcription regu
417	20	87.0	199	2	A71411	proteasome endopep	490	20	87.0	242	2	D98301	uxu operon regulat
418	20	87.0	200	2	AC0369	cytochrome C-type	491	20	87.0	242	2	AH2794	polyketide biosynt
419	20	87.0	200	2	B32477	prolactin II precu	492	20	87.0	242	2	G97573	frne protein VCA01
420	20	87.0	204	2	T51982	proteasome endopep	493	20	87.0	242	2	H69471	conserved hypotet
421	20	87.0	207	2	A60969	prolactin precursor	494	20	87.0	245	2	H90196	hypothetical prote
422	20	87.0	207	2	S21965	prolactin - silver	495	20	87.0	246	2	B95933	conserved hypotet
423	20	87.0	207	2	T29181	hypothetical prote	496	20	87.0	250	2	T35927	conserved hypotet
424	20	87.0	208	2	T26144	hypothetical prote	497	20	87.0	252	2	S67449	probable endonucle
425	20	87.0	209	2	S30541	prolactin precursor	498	20	87.0	254	1	VHUUUU	nucleocapsid prote
426	20	87.0	209	2	G71430	hypothetical prote	499	20	87.0	254	1	A64175	molybdate-binding
427	20	87.0	210	1	S01435	prolactin precursor	500	20	87.0	254	2	T05076	hypothetical prote
428	20	87.0	210	2	S151084	prolactin precursor	501	20	87.0	255	2	S04668	hypothetical prote
429	20	87.0	210	2	PN0092	prolactin precursor	502	20	87.0	255	2	C70750	hypothetical prote
430	20	87.0	210	2	S16765	prolactin precursor	503	20	87.0	255	2	D86693	conserved hypotet
431	20	87.0	210	2	A31364	prolactin precursor	504	20	87.0	256	2	S51050	hypothetical prote
432	20	87.0	210	2	S34351	prolactin precursor	505	20	87.0	257	1	C64812	molybdate-binding
433	20	87.0	210	2	S52475	prolactin - Atlant	506	20	87.0	257	2	G90727	molybdate-binding
434	20	87.0	210	2	S71486	prolactin precursor	507	20	87.0	257	2	H85578	molybdate-binding
435	20	87.0	210	2	D84273	fibrillarlin [impor	508	20	87.0	257	2	AC0595	molybdate-binding
436	20	87.0	210	2	AH2668	ABC transporter, m	509	20	87.0	257	2	AC1879	hypothetical prote
437	20	87.0	210	2	F97450	hypothetical prote	510	20	87.0	257	2	T29183	hypothetical prote
438	20	87.0	211	2	S00359	prolactin precursor	511	20	87.0	258	2	S16612	opacity protein op
439	20	87.0	211	2	H86852	hypothetical prote	512	20	87.0	258	2	F69479	nicotinate-nucleot
440	20	87.0	212	2	S151275	prolactin precursor	513	20	87.0	258	2	T05194	hypothetical prote
441	20	87.0	212	2	A32477	prolactin I precu	514	20	87.0	259	2	G75400	probable oxidoredu
442	20	87.0	212	2	S151034	prolactin-I - Moza	515	20	87.0	259	2	S41890	hypothetical prote
443	20	87.0	212	2	C70737	probable sigp prot	516	20	87.0	260	2	S16611	opacity protein op
444	20	87.0	213	2	T02697	hypothetical prote	517	20	87.0	260	2	T42960	hypothetical prote
445	20	87.0	215	2	C86818	hypothetical prote	518	20	87.0	261	2	AE3499	O-sialoglycoprotei
446	20	87.0	215	2	S18228	replication initia	519	20	87.0	261	2	AG3116	conserved hypotet
447	20	87.0	216	2	F71002	hypothetical prote	520	20	87.0	261	2	G69117	diphthine synthase
448	20	87.0	216	2	G75128	hypothetical prote	521	20	87.0	265	2	T35850	probable hydrolase
449	20	87.0	217	2	C37944	CAMP response elem	522	20	87.0	265	2	T33852	hypothetical prote
450	20	87.0	217	2	D96013	probable partial t	523	20	87.0	265	2	F98170	hypothetical prote
451	20	87.0	220	2	A95339	RNA binding protei	524	20	87.0	266	2	A48349	U128 protein - ate
452	20	87.0	220	2	T09108	CAMP response elem	525	20	87.0	266	2	D95373	hypothetical prote
453	20	87.0	220	2	S26685	Max-binding bHLH-Z	526	20	87.0	267	2	T22502	hypothetical prote
454	20	87.0	221	2	A45181	hypothetical prote	527	20	87.0	268	2	D86270	F21F33.14 protein
455	20	87.0	223	2	AF1345	hypothetical prote	528	20	87.0	269	2	B47112	growth response pr
456	20	87.0	223	2	A11715	hypothetical prote	529	20	87.0	269	2	AG6490	TCR V beta CRE-mot
457	20	87.0	224	2	S20463	siderophore biosyn	530	20	87.0	270	2	AG0916	probable hydrolase
458	20	87.0	224	2	I39875	siderophore biosyn	531	20	87.0	271	2	S12560	transcription fact
459	20	87.0	224	2	AL3595	frnE protein [impo	532	20	87.0	272	2	S59042	splicing factor SR
460	20	87.0	226	1	LCRT	prolactin precursor	533	20	87.0	272	2	G89758	conserved hypotet
461	20	87.0	226	2	A49159	prolactin - golden	534	20	87.0	272	2	G71849	amino acid ABC tra
462	20	87.0	227	1	LC8U	prolactin precursor	535	20	87.0	277	2	D64666	glutamine ABC tran
463	20	87.0	228	1	LCMS	prolactin precursor	536	20	87.0	278	2	JE0216	28k surface antiq
464	20	87.0	228	2	A61402	prolactin precursor	537	20	87.0	278	2	D70504	hypothetical prote
465	20	87.0	228	2	F97323	protein-disulfide	538	20	87.0	278	2	S36101	CAMP response elem
466	20	87.0	229	1	LCPG	prolactin precursor	539	20	87.0	279	2	A87360	hypothetical prote
467	20	87.0	229	2	A61133	prolactin precursor	540	20	87.0	280	1	A53419	2,3-dihydroxy-4-ph

541	20	87.0	280	2	H81237	phn0-related prote	614	20	87.0	336	2	S74462	hypothetical prote
542	20	87.0	280	2	F82010	hypothetical prote	615	20	87.0	336	2	B86463	AIgi-like protein,
543	20	87.0	281	2	T28857	hypothetical prote	616	20	87.0	338	2	E95244	glycerol-3-phospha
544	20	87.0	283	2	D98325	hypothetical prote	617	20	87.0	338	2	C98109	glycerol-3-phospha
545	20	87.0	284	2	F71613	hypothetical prote	618	20	87.0	339	2	T25142	hypothetical prote
546	20	87.0	284	2	AF0695	probable secreted	619	20	87.0	339	2	T25204	hypothetical prote
547	20	87.0	285	2	H85356	hypothetical prote	620	20	87.0	341	2	E96499	probable fructose
548	20	87.0	287	2	JE0220	28k surface antige	621	20	87.0	341	2	H90814	beta-N-acetylgluco
549	20	87.0	289	2	T08176	glucose-1-phosphat	622	20	87.0	341	2	S20827	CAMP response elem
550	20	87.0	290	2	S41555	TyA protein - years	623	20	87.0	341	2	S26686	CAMP response elem
551	20	87.0	290	2	S69841	TyA protein - years	624	20	87.0	341	2	A85674	beta-N-acetylgluco
552	20	87.0	292	2	B70721	hypothetical prote	625	20	87.0	341	2	H89500	protein T2A10.7 l
553	20	87.0	293	2	T31480	hypothetical prote	626	20	87.0	341	2	H64854	probable glucosida
554	20	87.0	295	2	C82558	bifunctional methy	627	20	87.0	341	2	AB0644	probable glycosyl
555	20	87.0	296	2	G97059	era G1Fase [import	628	20	87.0	343	2	D83718	glycoprotein endop
556	20	87.0	296	2	C81906	hypothetical prote	629	20	87.0	344	2	S22796	probable portal pr
557	20	87.0	296	2	G81111	conserved hypotet	630	20	87.0	344	2	UC5601	CAMP response elem
558	20	87.0	296	2	D82515	ketoreductase XF27	631	20	87.0	344	2	UC5602	CAMP response elem
559	20	87.0	298	2	F69119	cation efflux syst	632	20	87.0	345	2	E70794	probable heat choc
560	20	87.0	299	2	A95293	TRM17a probable tr	633	20	87.0	345	2	T02609	anthranilate phosp
561	20	87.0	300	1	TVZ2VW	protein kinase (EC	634	20	87.0	348	1	D24723	probable quinone o
562	20	87.0	300	1	TVZ292	protein kinase (EC	635	20	87.0	349	2	AB1715	oxidoreductase hom
563	20	87.0	300	1	A36855	protein kinase (EC	636	20	87.0	349	2	AG1344	oxidoreductase hom
564	20	87.0	300	2	H72171	H1R protein - vari	637	20	87.0	351	1	JSBYP1	centromere-binding
565	20	87.0	300	2	T28600	hypothetical prote	638	20	87.0	351	2	S25480	heat shock transcr
566	20	87.0	302	2	T37440	protein kinase - v	639	20	87.0	351	2	E87317	hypothetical prote
567	20	87.0	302	2	B35961	hypothetical 21k p	640	20	87.0	351	2	E87317	hypothetical prote
568	20	87.0	302	2	S69725	hypothetical prote	641	20	87.0	351	2	T01845	hypothetical prote
569	20	87.0	303	2	S49053	glucose-1-phosphat	642	20	87.0	353	2	D97295	probable pksII pro
570	20	87.0	303	2	A69542	conserved hypotet	643	20	87.0	354	2	S72958	hypothetical prote
571	20	87.0	304	2	D81815	hypothetical DNA-b	644	20	87.0	356	2	T19792	hypothetical prote
572	20	87.0	304	2	T16704	hypothetical prote	645	20	87.0	357	2	S35250	flagellar biosynth
573	20	87.0	305	2	A72636	hypothetical prote	646	20	87.0	357	2	QJ1292	hypothetical 39K p
574	20	87.0	307	2	B83167	hypothetical prote	647	20	87.0	358	2	A70746	hypothetical prote
575	20	87.0	308	1	A34082	branched-chain-ami	648	20	87.0	358	2	T17619	hypothetical prote
576	20	87.0	308	2	I48080	coatomer complex e	649	20	87.0	358	2	A96534	hypothetical prote
577	20	87.0	308	2	I46019	coatomer complex e	650	20	87.0	359	2	A96534	lipopolysaccharide
578	20	87.0	308	2	T40266	probable ras relat	651	20	87.0	360	2	B72359	conserved hypotet
579	20	87.0	309	1	XNECV	branched-chain-ami	652	20	87.0	360	2	D71323	probable LacI-fami
580	20	87.0	309	2	H91216	branched-chain ami	653	20	87.0	360	2	H95401	gibberellin 20-dio
581	20	87.0	309	2	A86063	branched-chain ami	654	20	87.0	361	2	T06330	methyellated-DNA- [pr
582	20	87.0	309	2	AD0924	branched-chain ami	655	20	87.0	361	2	AH3446	probable 3-dehydro
583	20	87.0	309	2	T18579	cyclophilin isofo	656	20	87.0	361	2	F86973	probable 3-dehydro
584	20	87.0	311	2	H69994	cysteine synthase	657	20	87.0	361	2	T42525	splicing factor-1i
585	20	87.0	312	2	G84058	cysteine synthase	658	20	87.0	362	1	S17768	3-dehydroquinatase
586	20	87.0	312	2	T35742	hypothetical prote	659	20	87.0	363	2	S60684	adenylate cyclase
587	20	87.0	313	2	AH3058	2-HYDROXY-3-OXOPRO	660	20	87.0	363	2	B83023	hypothetical prote
588	20	87.0	313	2	H98227	3-hydroxyisobutyla	661	20	87.0	364	1	PAQXF	fructose-bisphosph
589	20	87.0	313	2	H84938	flagellar motor sw	662	20	87.0	364	2	B87124	conserved hypotet
590	20	87.0	315	2	T50561	SINAI protein [imp	663	20	87.0	364	2	T34713	hypothetical prote
591	20	87.0	315	2	H96598	protein F20N2.8 [i	664	20	87.0	365	2	T06991	gibberellin 20-dio
592	20	87.0	315	2	B82229	hypothetical prote	665	20	87.0	365	2	T06990	gibberellin 20-dio
593	20	87.0	316	2	T01771	hypothetical prote	666	20	87.0	365	2	G83373	hypothetical prote
594	20	87.0	317	1	JC4827	protein kinase (EC	667	20	87.0	365	2	T37730	probable pre-mRNA
595	20	87.0	317	2	A13535	penicillin amidase	668	20	87.0	365	2	A71410	hypothetical prote
596	20	87.0	317	2	S54548	hypothetical prote	669	20	87.0	367	2	S72924	hypothetical prote
597	20	87.0	318	2	S37648	hypothetical prote	670	20	87.0	369	2	F84229	probable peptidase
598	20	87.0	321	2	G71468	probable fa/phosph	671	20	87.0	369	2	F81178	histone deacetylase
599	20	87.0	321	2	T31847	hypothetical prote	672	20	87.0	369	2	H75461	sensor histidine k
600	20	87.0	322	2	D72733	conserved hypotet	673	20	87.0	370	2	G87212	conserved hypotet
601	20	87.0	322	2	S42426	aspartate-semialde	674	20	87.0	370	2	I38177	ras-related G1Pase
602	20	87.0	325	2	E75404	ABC transporter, A	675	20	87.0	374	2	AC3569	glucuronate isomer
603	20	87.0	326	2	E95941	probable NADPH2:qu	676	20	87.0	375	2	T32251	hypothetical prote
604	20	87.0	327	2	A12677	quinone oxidoreduc	677	20	87.0	379	2	AB0959	hypothetical prote
605	20	87.0	327	2	F97835	beta-glucosidase (	678	20	87.0	381	2	G83518	probable acyl-CoA
606	20	87.0	328	2	T07045	hypothetical prote	679	20	87.0	381	2	B82840	conserved hypotet
607	20	87.0	329	2	B84199	hypothetical prote	680	20	87.0	382	2	F87464	hypothetical prote
608	20	87.0	330	2	H70500	probable moeX prot	681	20	87.0	383	2	T22752	hypothetical prote
609	20	87.0	331	1	C69026	acetylpolymine am	682	20	87.0	385	2	G84459	probable GDP-manno
610	20	87.0	332	2	D70605	probable rhoA prot	683	20	87.0	385	2	A11926	hypothetical prote
611	20	87.0	333	2	H89961	hypothetical prote	684	20	87.0	386	2	T26108	hypothetical prote
612	20	87.0	334	2	T33201	hypothetical prote	685	20	87.0	389	2	E86634	hypothetical prote
613	20	87.0	335	2	G96607	probable galactino	686	20	87.0	391	2	G84278	X-pro aminopeptida

687	20	87.0	396	2	S56496	prophage P4 integr	760	20	87.0	482	2	B83113	catalase PA4236 [i
688	20	87.0	397	2	B70048	conserved hypotet	761	20	87.0	482	2	A83655	lysine decarboxyla
689	20	87.0	398	1	S47520	vitamin D-3 25-hyd	762	20	87.0	483	2	S37055	catalase (EC 1.11.
690	20	87.0	398	1	XUECGA	glycine C-acetyltr	763	20	87.0	483	2	JH0532	catalase (EC 1.11.
691	20	87.0	398	2	G91190	2-amino-3-ketobuty	764	20	87.0	484	2	A58663	catalase (EC 1.11.
692	20	87.0	398	2	H86037	glycine C-acetyltr	765	20	87.0	485	2	A70706	probable phoR prot
693	20	87.0	398	2	A10973	glycine C-acetyltr	766	20	87.0	485	2	S73333	MG260 homolog - My
694	20	87.0	400	2	S76929	hypothetical prote	767	20	87.0	487	2	T34858	catalase (EC 1.11.
695	20	87.0	400	2	A97535	ispD/ispF bifuncti	768	20	87.0	489	1	VGXPMV	surface glycoprote
696	20	87.0	400	2	AC2754	ISP/ISPf bifuncti	769	20	87.0	490	2	C72317	conserved hypotet
697	20	87.0	403	2	B35401	cytochrome P450 10	770	20	87.0	492	1	E69114	conserved hypotet
698	20	87.0	403	2	S02836	site-specific DNA-	771	20	87.0	492	1	S32491	conserved hypotet
699	20	87.0	404	2	AH0803	3-oxoacyl-[acyl-ca	772	20	87.0	494	2	B89870	testosterone 7alph
700	20	87.0	404	2	S59589	starvation-sensing	773	20	87.0	494	2	H82489	hypothetical prote
701	20	87.0	404	2	AG0679	starvation sensing	774	20	87.0	494	2	H23525	conserved hypotet
702	20	87.0	405	2	G95903	hypothetical prote	775	20	87.0	499	2	A55227	hypothetical prote
703	20	87.0	406	1	SVECA1	3-oxoacyl-[acyl-ca	776	20	87.0	500	2	T24901	catalase (EC 1.11.
704	20	87.0	406	2	G91029	3-oxoacyl-[acyl-ca	777	20	87.0	500	2	A29487	hypothetical prote
705	20	87.0	406	2	H85873	3-oxoacyl-[acyl-ca	778	20	87.0	501	2	A34236	cytochrome P450 3A
706	20	87.0	406	2	T28957	hypothetical prote	779	20	87.0	501	2	JC4702	cytochrome P450 3A
707	20	87.0	406	2	S72894	exopolysphatase	780	20	87.0	503	2	H71659	transcription term
708	20	87.0	406	2	AF2531	transposase alr735	781	20	87.0	504	2	A29410	cytochrome P450, g
709	20	87.0	406	2	AI2515	transposase alr730	782	20	87.0	504	2	SS0892	cytochrome P450 3A
710	20	87.0	409	2	T11743	p47 protein - pig	783	20	87.0	507	2	AD3621	catalase (EC 1.11.
711	20	87.0	413	2	JC8001	N-acetylglactosam	784	20	87.0	514	2	A45228	25-hydroxyvitamin
712	20	87.0	415	2	JC7167	C kinase 1 interac	785	20	87.0	514	2	C36901	chorion transcript
713	20	87.0	415	2	C70552	hypothetical prote	786	20	87.0	515	1	CSBYP	catalase (EC 1.11.
714	20	87.0	415	2	B83634	hypothetical prote	787	20	87.0	515	2	AE0186	probable decarboxy
715	20	87.0	416	2	I51096	thyroid hormone re	788	20	87.0	522	2	AB2928	hypothetical prote
716	20	87.0	416	2	A56486	perinuclear bindin	789	20	87.0	522	2	E98354	hypothetical prote
717	20	87.0	421	2	B82062	conserved hypotet	790	20	87.0	523	2	C70717	aliqui (AB011415) l
718	20	87.0	421	2	B71463	probable im protei	791	20	87.0	523	2	G96809	probable purH prot
719	20	87.0	422	1	JC1210	polyketide beta-ke	792	20	87.0	523	2	G96777	protein F28K19.28
720	20	87.0	422	2	T24775	hypothetical prote	793	20	87.0	526	1	TVFVR	hypothetical prote
721	20	87.0	427	2	A84820	hypothetical prote	794	20	87.0	526	1	OKFVTR	protein-tyrosine k
722	20	87.0	428	2	S76384	hypothetical prote	795	20	87.0	526	2	S15582	protein-tyrosine k
723	20	87.0	429	2	AD1921	hypothetical prote	796	20	87.0	526	2	S20808	protein-tyrosine k
724	20	87.0	430	2	B87097	probable conserved	797	20	87.0	526	2	S26420	protein-tyrosine k
725	20	87.0	430	2	C86346	FlaF4.3 protein -	798	20	87.0	526	2	T39748	probable ser/thr p
726	20	87.0	431	2	T11854	protein kinase (EC	799	20	87.0	526	2	D96014	probable sugar upt
727	20	87.0	434	2	F84332	succinoglycan bios	800	20	87.0	527	2	T45439	probable phosphori
728	20	87.0	435	2	T24477	hypothetical prote	801	20	87.0	527	2	B55415	rhomogalacturonas
729	20	87.0	435	2	T19687	hypothetical prote	802	20	87.0	531	2	T35226	nitrate reductase
730	20	87.0	437	2	S07040	alpha-amylase (EC	803	20	87.0	531	2	B84492	probable retroelem
731	20	87.0	437	2	T26767	hypothetical prote	804	20	87.0	534	2	F84398	hypothetical prote
732	20	87.0	438	1	ALBH	alpha-amylase (EC	805	20	87.0	534	2	P84398	phosphate ABC tran
733	20	87.0	440	2	JC2532	secretin receptor	806	20	87.0	538	2	A54391	translation initia
734	20	87.0	440	2	A82369	thiamin-phosphate	807	20	87.0	542	2	T29835	sphingosine-i-phos
735	20	87.0	443	2	JQ1327	alpha-amylase (EC	808	20	87.0	546	2	T48520	hypothetical prote
736	20	87.0	444	2	TS0931	conserved hypotet	809	20	87.0	547	2	A40656	hypothetical prote
737	20	87.0	444	2	B83249	hypothetical prote	810	20	87.0	547	2	AE1022	probable membrane
738	20	87.0	444	2	T27863	alpha-amylase (EC	811	20	87.0	549	2	C72387	hypothetical prote
739	20	87.0	445	2	S19990	conserved hypotet	812	20	87.0	554	2	T15992	hypothetical prote
740	20	87.0	446	2	B82975	glycine dehydrogen	813	20	87.0	556	2	C89181	protein C51B3.7b l
741	20	87.0	448	2	A69959	probable MFS trans	814	20	87.0	557	2	AD2832	DNA repair protein
742	20	87.0	448	2	H83335	hypothetical prote	815	20	87.0	557	2	H97609	DNA repair protein
743	20	87.0	448	2	S57686	hypothetical prote	816	20	87.0	557	2	S56342	yidB protein - Esc
744	20	87.0	451	2	F84492	probable Athila re	817	20	87.0	557	2	H91265	hypothetical prote
745	20	87.0	451	2	A36908	spore cortex penic	818	20	87.0	557	2	E86106	yidB protein [simi
746	20	87.0	452	2	JC4038	47K glycoprotein p	819	20	87.0	562	2	T05758	hypothetical prote
747	20	87.0	453	2	F89720	protein R1010.2 l	820	20	87.0	567	2	F82384	probable phosphoma
748	20	87.0	458	2	T27217	hypothetical prote	821	20	87.0	571	2	T26638	hypothetical prote
749	20	87.0	460	2	C96736	probable ketoacyl-	822	20	87.0	573	2	A41319	3-oxosteroid 1-deh
750	20	87.0	467	2	H82152	PTS system, fructo	823	20	87.0	573	2	C64611	hypothetical prote
751	20	87.0	469	2	B95958	probable glucurona	824	20	87.0	574	2	T14162	hABC transport pro
752	20	87.0	471	2	T34956	probable UDP-N-ace	825	20	87.0	575	2	S59740	NHDI protein - yea
753	20	87.0	472	2	AE1955	two-component sens	826	20	87.0	575	2	T45668	hypothetical prote
754	20	87.0	473	2	D96591	hypothetical prote	827	20	87.0	575	2	S62713	phytochrome la - M
755	20	87.0	476	2	B71696	probable transport	828	20	87.0	578	2	S51379	pyruvate phosphoge
756	20	87.0	480	1	B70804	DNA repair protein	829	20	87.0	580	2	T34668	pyruvate dehydroge
757	20	87.0	480	2	JC7672	catalase (EC 1.11.	830	20	87.0	581	1	FVEBT	DNA primase (EC 2.
758	20	87.0	481	2	T28900	hypothetical prote	831	20	87.0	583	2	S17671	protein-tyrosine-p
759	20	87.0	482	2	S49465	catalase (EC 1.11.	832	20	87.0	585	2	S15963	hypothetical prote



833	20	87.0	586	1	ORXLE	estrogen receptor	906	20	87.0	693	1	TNBEF7	73.8K alpha trans-
834	20	87.0	586	2	B84271	glutamyl-tRNA synt	907	20	87.0	694	2	T30725	probable abortive
835	20	87.0	586	2	T39769	trp-asp repeats co	908	20	87.0	698	2	T32840	hypothetical prote
836	20	87.0	586	2	AD2493	hypothetical prote	909	20	87.0	699	2	C96655	hypothetical prote
837	20	87.0	589	1	QRCHE	estrogen receptor	910	20	87.0	701	2	S64737	80K estrogen recep
838	20	87.0	590	2	B85010	hypothetical prote	911	20	87.0	706	1	WZBED8	gene 45 protein -
839	20	87.0	590	2	S63193	hypothetical prote	912	20	87.0	712	2	AB2776	DNA gyrase subunit b
840	20	87.0	591	2	C84220	propionyl-CoA carb	913	20	87.0	712	2	H97555	DNA gyrase chain b
841	20	87.0	592	2	S43570	COSB5.6 protein (c	914	20	87.0	719	1	MNKR3D	nonstructural prot
842	20	87.0	595	1	QRHUE	estrogen receptor	915	20	87.0	721	2	F82198	probable toxin sec
843	20	87.0	595	1	QRMSE	estradiol receptor	916	20	87.0	723	1	S30105	tryptophan 2-mono
844	20	87.0	599	1	AG1964	estrogen receptor	917	20	87.0	724	2	C49423	semaphorin II prec
845	20	87.0	601	1	QRTE	hypothetical prote	918	20	87.0	724	2	D85075	probable athila tr
846	20	87.0	601	1	QRTE	hypothetical prote	919	20	87.0	728	2	S55601	hypothetical prote
847	20	87.0	601	2	A28577	estrogen receptor	920	20	87.0	730	2	AI3480	penicillin-binding
848	20	87.0	601	2	D96001	NADPH-ferrihemopro	921	20	87.0	733	2	S78376	photosystem I P700
849	20	87.0	601	2	T00119	probable 1,4-alpha	922	20	87.0	733	2	F84476	probable Ahila re
850	20	87.0	602	2	T45386	probable transcrip	923	20	87.0	734	2	C69691	GRP pyrophosphokin
851	20	87.0	604	2	S57784	endopeptidase IV [	924	20	87.0	734	2	S73206	photosystem I prot
852	20	87.0	604	2	S25203	MTG8 protein splic	925	20	87.0	735	2	G02937	feritin beta - cr
853	20	87.0	606	2	T13152	srM8 protein - Str	926	20	87.0	738	2	AC1265	(p)ppGpp synthetas
854	20	87.0	609	2	S28283	WDR1 protein - hum	927	20	87.0	738	2	AE1627	(p)ppGpp synthetas
855	20	87.0	610	2	T16194	hypothetical prote	928	20	87.0	749	2	I39708	tryptophan 2-mono
856	20	87.0	614	1	S43237	hypothetical prote	929	20	87.0	752	4	S57784	AMLI/MTG8 mutant f
857	20	87.0	617	2	T29660	2-methyleneglutar	930	20	87.0	754	2	S60464	mes-3 protein - Ca
858	20	87.0	618	2	S11445	hypothetical prote	931	20	87.0	754	2	G87767	protein mes-3 [imp
859	20	87.0	619	2	D90072	parasporal crystal	932	20	87.0	755	1	DAAGWT	tryptophan 2-mono
860	20	87.0	620	2	T10423	hypothetical prote	933	20	87.0	755	1	QAG4T	tryptophan 2-mono
861	20	87.0	620	2	E84481	estrogen receptor	934	20	87.0	755	2	AI3228	tryptophan 2-mono
862	20	87.0	623	2	G70644	probable protein k	935	20	87.0	758	2	E83884	hypothetical prote
863	20	87.0	623	2	A48315	probable spA prot	936	20	87.0	759	2	AE1314	pyruvate formate-1
864	20	87.0	625	2	H70330	lamin III - Africa	937	20	87.0	759	2	AE1686	pyruvate formate-1
865	20	87.0	625	2	T20634	hypothetical prote	938	20	87.0	761	2	S46611	YTA10 protein - ye
866	20	87.0	629	2	T06675	hypothetical prote	939	20	87.0	763	2	A88881	hypothetical prote
867	20	87.0	630	2	F85074	hypothetical prote	940	20	87.0	765	1	ISHUT1	DNA topoisomerase
868	20	87.0	634	2	T27881	hypothetical prote	941	20	87.0	767	1	WMBEP6	ribonucleoside-dip
869	20	87.0	638	2	T20944	hypothetical prote	942	20	87.0	767	2	JU0144	DNA topoisomerase
870	20	87.0	639	2	C83624	probable two-compo	943	20	87.0	767	2	A49546	DNA topoisomerase
871	20	87.0	639	2	T43190	probable actin-bin	944	20	87.0	768	2	A82009	DNA topoisomerase
872	20	87.0	639	2	AI2663	potassium uptake p	945	20	87.0	768	2	H81236	DNA topoisomerase
873	20	87.0	639	2	H97445	potassium uptake p	946	20	87.0	770	1	WZBE30	gene 30 protein -
874	20	87.0	640	2	S52047	deoxyribodipyrimid	947	20	87.0	772	2	A48822	protein-glutamine
875	20	87.0	644	2	B71515	probable tail-spec	948	20	87.0	775	2	T38352	hypothetical prote
876	20	87.0	645	2	T27186	hypothetical prote	949	20	87.0	776	2	T15411	hypothetical prote
877	20	87.0	648	2	F82290	soluble lytic mure	950	20	87.0	780	1	WMBEH8	infected cell prot
878	20	87.0	649	2	T01106	hypothetical prote	951	20	87.0	782	2	E90427	hypothetical prote
879	20	87.0	649	2	B81673	tail specific prot	952	20	87.0	783	2	T00782	probable anthranil
880	20	87.0	650	2	S64939	CDC45 protein - ye	953	20	87.0	785	1	WMBEK8	infected cell prot
881	20	87.0	652	2	T20131	proprotein convert	954	20	87.0	785	1	WMBEW8	infected cell prot
882	20	87.0	652	2	T10576	hypothetical prote	955	20	87.0	786	2	E87565	conserved hypotet
883	20	87.0	655	2	T16538	hypothetical prote	956	20	87.0	786	2	T33856	hypothetical prote
884	20	87.0	656	2	D82388	glycogen operon pr	957	20	87.0	788	2	B84857	hypothetical prote
885	20	87.0	657	2	T49875	probable amidase -	958	20	87.0	792	2	A70476	ATP-dependent DNA
886	20	87.0	660	2	S50383	gamma-glutamyltran	959	20	87.0	792	2	AC3619	transketolase (EC
887	20	87.0	662	2	G95929	probable methylcro	960	20	87.0	796	2	T34805	hypothetical prote
888	20	87.0	664	1	TNBE70	70.5K alpha trans-	961	20	87.0	802	2	C86303	probable vacuolar
889	20	87.0	668	2	AC1337	transcription anti	962	20	87.0	803	1	RGBYW6	regulatory protein
890	20	87.0	668	2	AH1707	transcription anti	963	20	87.0	803	2	H87197	penicillin binding
891	20	87.0	670	2	T00083	hypothetical prote	964	20	87.0	806	2	T13551	hypothetical prote
892	20	87.0	672	2	T25876	hypothetical prote	965	20	87.0	825	1	EDBEXD	immediate-early pr
893	20	87.0	674	2	S74506	ribonuclease E - S	966	20	87.0	826	2	E96720	probable alpha-amy
894	20	87.0	675	2	F87022	penicillin-binding	967	20	87.0	829	2	S72366	DNA topoisomerase
895	20	87.0	677	1	ADPG04	NADPH-ferrihemopro	968	20	87.0	833	2	S48558	probable membrane
896	20	87.0	677	2	A60557	NADPH-ferrihemopro	969	20	87.0	834	2	B82940	conserved hypotet
897	20	87.0	678	1	RDRT04	NADPH-ferrihemopro	970	20	87.0	835	2	T47521	respiratory burst
898	20	87.0	678	2	S27158	NADPH-ferrihemopro	971	20	87.0	835	2	A88238	protein Tl3H5.4 [i
899	20	87.0	679	2	A25505	NADPH-ferrihemopro	972	20	87.0	836	1	S25218	outer membrane ush
900	20	87.0	683	2	JH0810	guanylate cyclase	973	20	87.0	841	2	G71814	hypothetical prote
901	20	87.0	684	2	T49436	hypothetical prote	974	20	87.0	842	2	S51513	phosphoribosyl-AMP
902	20	87.0	687	2	E69733	PBSX prophage ORF	975	20	87.0	844	2	F86231	hypothetical prote
903	20	87.0	688	2	S32961	hypothetical prote	976	20	87.0	844	2	G64704	hypothetical prote
904	20	87.0	691	2	E70906	probable beta-gluc	977	20	87.0	865	2	A83946	DNA mismatch repai
905	20	87.0	692	2	T21722	hypothetical prote	978	20	87.0	865	2	T09050	AC133 antigen - hu

979 20 87.0 865 2 AB05322  
 980 20 87.0 866 2 B85075  
 981 20 87.0 868 2 G54119  
 982 20 87.0 869 1 A28443  
 983 20 87.0 880 2 E69680  
 984 20 87.0 880 2 S51473  
 985 20 87.0 884 2 C70729  
 986 20 87.0 888 2 C90595  
 987 20 87.0 890 2 A48753  
 988 20 87.0 893 2 S63378  
 989 20 87.0 893 2 D81989  
 990 20 87.0 904 2 C83030  
 991 20 87.0 905 2 T40015  
 992 20 87.0 910 2 C86615  
 993 20 87.0 910 2 F72009  
 994 20 87.0 915 2 T26695  
 995 20 87.0 920 1 D48349  
 996 20 87.0 921 2 G02326  
 997 20 87.0 926 2 S36742  
 998 20 87.0 927 2 T47827  
 999 20 87.0 929 2 T32492  
 1000 20 87.0 950 2 T38777

## ALIGNMENTS

## RESULT 1

hypothetical protein NMA1220 [imported] - Neisseria meningitidis (strain Z2491 serogroup C81890)  
 C:Species: Neisseria meningitidis  
 C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
 C:Accession: C81890  
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holroyd, S.; Jagers, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandream, M.A.; Barrell, D.G.; Whitehead, S.; Barrett, T.; Haywood, J.; Davis, P.; Dougan, G.; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Stevens, K.; Whitehead, S.; Barrett, T.; Skelton, J.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, T.; Nature 404, 502-506, 2000  
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
 A:Reference number: A81775; MUID:2022556; PMID:10761919  
 A:Accession: C81890  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-87 <PAR>  
 A:Cross-references: GB:AL162755; GB:AL157959; NID:G7379742; PIDN:CAB84480.1; PID:G737990  
 A:Experimental source: serogroup A, strain Z2491  
 C:Genetics:  
 A:Gene: NMA1220

Query Match 100.0%; Score 23; DB 2; Length 87;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 ||||  
 Db 46 DAHK 49

## RESULT 2

T44734  
 hypothetical protein MLCB1450.18 [imported] - Mycobacterium leprae  
 C:Species: Mycobacterium leprae  
 C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000  
 C:Accession: T44734  
 R:James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, January 1998  
 A:Reference number: Z22831  
 A:Accession: T44734  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-92 <JAM>  
 A:Cross-references: EMBL:AL035159; PIDN:CAA22702.1  
 A:Experimental source: cosmid B1450  
 C:Genetics:  
 A:Note: MLCB1450.18

Query Match 100.0%; Score 23; DB 2; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 ||||  
 Db 41 DAHK 44

## RESULT 3

AH0375  
 hypothetical protein YPO3089 [imported] - Yersinia pestis (strain CO92)  
 C:Species: Yersinia pestis  
 C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
 C:Accession: AH0375  
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Stevens, K.; Whitehead, S.; Barrett, T.; Skelton, J.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, T.; Nature 413, 523-527, 2001  
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A:Reference number: AB0001; MUID:21470413; PMID:11586360  
 A:Accession: AH0375  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-94 <KUR>  
 A:Cross-references: GB:AL590842; PIDN:CAC92331.1; PID:GL5981042; GSPDB:GN00175  
 C:Genetics:  
 A:Gene: YPO3089

Query Match 100.0%; Score 23; DB 2; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 ||||  
 Db 19 DAHK 22

## RESULT 4

G86805  
 transcription regulator [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
 C:Species: Lactococcus lactis subsp. lactis  
 C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
 C:Accession: G86805  
 R:Boletín, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich, S.; Bolotin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich, S.; Genome Res. 11, 731-753, 2001  
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis subsp. lactis strain IL1403.  
 A:Reference number: A86625; MUID:21235186; PMID:11337471  
 A:Accession: G86805  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-100 <STO>  
 A:Cross-references: GB:AF005176; PID:GL2724437; PIDN:AAK05545.1; GSPDB:GN00146  
 A:Experimental source: strain IL1403  
 C:Genetics:  
 A:Gene: yogl

Query Match 100.0%; Score 23; DB 2; Length 100;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 ||||  
 Db 18 DAHK 21

## RESULT 5

E75528  
 hypothetical protein - Deinococcus radiodurans (strain R1)  
 C:Species: Deinococcus radiodurans  
 C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
 C:Accession: E75528

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
 , M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zaleski, C.; Ma  
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999  
 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
 A;Reference number: A75250; MUID:20036896; PMID:10567266  
 A;Accession: E75528  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-102 <WHI>  
 A;Cross-references: GB:AE001896; GB:AE000513; NID:G6458032; PIDN:AAF09945.1; PID:G645804  
 A;Experimental source: strain R1  
 C;Genetics:  
 A;Gene: DR0355  
 A;Map position: 1

Query Match 100.0%; Score 23; DB 2; Length 102;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 Db 49 DAHK 52

RESULT 6

G43258  
 phosphotransferase system enzyme II (EC 2.7.1.69), lactose-specific, factor III - Strept  
 N;Alternate names: phosphotransferase system enzyme III, lactose-specific  
 C;Species: Streptococcus mutans  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 24-Nov-2003  
 C;Accession: G43258; S27705  
 R;Rosey, E.L.; Stewart, G.C.  
 J. Bacteriol. 174, 6159-6170, 1992  
 A;Title: Nucleotide and deduced amino acid sequences of the lacR, lacABCD, and lacPE gen  
 onents of the lactose operon of Streptococcus mutans.  
 A;Reference number: A43258; MUID:93015655; PMID:1400164  
 A;Accession: G43258  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-104 <ROS>  
 A;Cross-references: EMBL:M80797; NID:G153671; PIDN:AAA26908.1; PID:G153677  
 A;Note: sequence extracted from NCBI backbone (NCBIP:115206)  
 C;Genetics:  
 A;Gene: lacF  
 C;Superfamily: phosphotransferase system lactose/cellobiose-specific enzyme II,  
 C;Keywords: phosphoprotein; phosphotransferase

Query Match 100.0%; Score 23; DB 1; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 Db 52 DAHK 55

RESULT 7

T45101  
 H+-transporting two-sector ATPase (EC 3.6.3.14) chain H [imported] - Methanosarcina maze  
 C;Species: Methanosarcina mazei  
 C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 03-Jun-2002  
 R;Accession: T45101  
 R;Ruppert, C.; Wimmers, S.; Muller, V.  
 submitted to the EMBL Data Library, March 1998  
 A;Reference number: Z22913  
 A;Accession: T45101  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-109 <RUP>  
 A;Cross-references: EMBL:U47274; PIDN:AAC06380.1  
 A;Experimental source: strain Gol  
 C;Genetics:

A;Gene: ahaH  
 C;Keywords: hydrolase

Query Match 100.0%; Score 23; DB 2; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 Db 49 DAHK 52

## RESULT 8

G97473

hypothetical protein AGR\_C\_1710 [imported] - Agrobacterium tumefaciens (strain C58, Cere  
 C;Species: Agrobacterium tumefaciens  
 C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
 C;Accession: G97473  
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,  
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;  
 Science 294, 2323-2328, 2001  
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
 A;Reference number: A97359; MUID:21608551; PMID:11743194  
 A;Accession: G97473  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-112 <KUR>  
 A;Cross-references: GB:AE007869; PIDN:AAK86744.1; PID:G15155938; GSPDB:GN00169  
 C;Genetics:  
 A;Gene: AGR\_C\_1710  
 A;Map position: circular chromosome

Query Match 100.0%; Score 23; DB 2; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 Db 84 DAHK 87

## RESULT 9

C82906

ribosome binding factor A UU321 [imported] - Ureaplasma urealyticum  
 C;Species: Ureaplasma urealyticum  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C;Accession: C82906  
 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.  
 submitted to GenBank, February 2000  
 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir  
 A;Reference number: A82870  
 A;Accession: C82906  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-116 <GLA>  
 A;Cross-references: GB:AE002129; GB:AF222894; NID:G6899292; PIDN:AAF30730.1; GSPDB:GN001  
 A;Experimental source: serovar 3; biovar 1  
 C;Genetics:  
 A;Gene: rbfA; UU321  
 A;Genetic code: SGC3

Query Match 100.0%; Score 23; DB 2; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 Db 53 DAHK 56

## RESULT 10

B90155

hypothetical protein SS00150 [imported] - Sulfolobus solfataricus

C;Species: Sulfolobus solfataricus  
 C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
 C;Accession: B90155  
 R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-  
 Jorg, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.  
 submitted to GenBank, April 2001  
 A;Description: Sulfolobus solfataricus complete genome.  
 A;Reference number: A99139  
 A;Accession: B90155  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-118 <KUR>  
 A;Cross-references: GB:AE006641; NID:gl13813279; PIDN:AAK40497.1; GSPDB:GN00155  
 C;Genetics:  
 A;Gene: SS00150

Query Match 100.0%; Score 23; DB 2; Length 118;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 ||||  
 Db 85 DAHK 88

## RESULT 11

T36836

hypothetical protein SCI35.23 - Streptomyces coelicolor

C;Species: Streptomyces coelicolor  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 04-Mar-2000  
 C;Accession: T36836  
 R;Oliver, K.; Harris, D.; Parkhill, J.; Barrrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, September 1998

A;Reference number: Z21615

A;Accession: T36836

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-121 <OLI>

A;Cross-references: EMBL:AL031541; PIDN:CAA20812.1; GSPDB:GN00070; SCOEDB:SCI35.23

A;Experimental source: strain A3(2)

C;Genetics:

A;Gene: SCOEDB:SCI35.23

C;Superfamily: Streptomyces coelicolor hypothetical protein SCI35.23

Query Match 100.0%; Score 23; DB 2; Length 121;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 ||||  
 Db 52 DAHK 55

## RESULT 12

C70965

hypothetical protein Rv2647 - Mycobacterium tuberculosis (strain H37RV)

C;Species: Mycobacterium tuberculosis

C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999

C;Accession: C70965

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A;Reference number: A70500; MUID:9829598; PMID:9634230

A;Accession: C70965

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-122 <COL>

A;Cross-references: GB:Z80225; GB:AL123456; NID:g3242265; PIDN:CAB02355.1; PID:e266520;

A;Experimental source: strain H37RV

C;Genetics:  
 A;Gene: Rv2647

Query Match 100.0%; Score 23; DB 2; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 ||||  
 Db 78 DAHK 81

## RESULT 13

C75371

conserved hypothetical protein - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000

C;Accession: C75371

R;White, O.; Eissen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.

, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: C75371

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-122 <WHI>

A;Cross-references: GB:AE002007; GB:AE000513; NID:g6459402; PIDN:AAF11196.1; PID:g64594

A;Experimental source: strain R1

C;Genetics:

A;Gene: DR1636

A;Map position: 1

Query Match 100.0%; Score 23; DB 2; Length 122;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 ||||  
 Db 68 DAHK 71

## RESULT 14

T06427

aminopeptidase - tomato (fragment)

C;Species: Lycopersicon esculentum (tomato)

C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 08-Oct-1999

C;Accession: T06427

R;Aggelis, A.; Kanellis, A.K.

submitted to the EMBL Data Library, March 1998

A;Description: Isolation and expression studies of tomato aminopeptidase under low oxyg

A;Reference number: Z15671

A;Accession: T06427

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-124 <AGG>

A;Cross-references: EMBL:AJ004922; NID:el284297; PIDN:CAA06222.1; PID:el284298

A;Experimental source: cultivar Ailsa Craig

C;Genetics:

A;Gene: AMP

Query Match 100.0%; Score 23; DB 2; Length 124;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 ||||  
 Db 94 DAHK 97

## RESULT 15

D81138

succinate dehydrogenase, cytochrome b556 chain NMB0948 [imported] - Neisseria meningitidis  
 C:Species: Neisseria meningitidis  
 C>Date: 31-Mar-2000 #sequence revision 31-Mar-2000 #text\_change 02-Feb-2001  
 C:Accession: D81138; B81881  
 R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
 ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.  
 Science 287, 1809-1815, 2000  
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.  
 A:Reference number: A81000; MUID:2017555; PMID:10710307  
 A:Accession: D81138  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-125 <TET>  
 A:Cross-references: GB:AE002446; GB:AE002098; NID:g7226185; PIDN:AAF41354.1; PID:g722618  
 A:Experimental source: serogroup B, strain MCS8  
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
 ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
 Nature 404, 502-506, 2000  
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
 A:Reference number: A81775; MUID:2022556; PMID:10761919  
 A:Accession: B81881  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-125 <PAR>  
 A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84405.1; PID:g737983  
 A:Experimental source: serogroup A, strain Z2491  
 C:Genetics:  
 C:Gene: sdhC; NMB0948; NMA1143  
 C:Superfamily: succinate dehydrogenase 14K hydrophobic protein

Query Match 100.0%; Score 23; DB 2; Length 125;  
 Best Local Similarity 100.0%; Pred. NO. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DAHK 4  
 Db 92 DAHK 95

Search completed: September 9, 2004, 23:48:23  
 Job time : 62 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 9, 2004, 23:33:02 ; Search time 23 Seconds

(without alignments)  
9.056 Million cell updates/sec

Title: US-10-076-071-1

Perfect score: 23

Sequence: 1 DAHK 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	104	1	PTLA_STRUM
2	23	100.0	107	1	Y210_COREF
3	23	100.0	107	1	Q9pql1 corynebacte
4	23	100.0	116	1	RBFA_UREPA
5	23	100.0	140	1	HBB_RANES
6	23	100.0	149	1	FUR_VIBPA
7	23	100.0	149	1	FUR_VIBVU
8	23	100.0	151	1	HUTP_BACSU
9	23	100.0	156	1	ATPF_VIBVU
10	23	100.0	168	1	LCRH_YERPE
11	23	100.0	168	1	LCRH_YERPS
12	23	100.0	170	1	PHAF_CVACA
13	23	100.0	178	1	IPYR_BRAJA
14	23	100.0	196	1	SODF_TETPY
15	23	100.0	205	1	UBAL_CANAL
16	23	100.0	207	1	VG66_BPMLS
17	23	100.0	207	1	YAFE_ECOLI
18	23	100.0	210	1	GTPI_BURBU
19	23	100.0	222	1	FSA_STREN
20	23	100.0	223	1	DEOC_MYCCE
21	23	100.0	224	1	DEOC_MYCPA
22	23	100.0	229	1	SOML_CYCLU
23	23	100.0	230	1	SOML_CARAU
24	23	100.0	230	1	SOML_HIPHI
25	23	100.0	230	1	SOML_ICTPU
26	23	100.0	231	1	SOML_SOLSE
27	23	100.0	231	1	SOML_SPAAU
28	23	100.0	231	1	SOML_SPAUL
29	23	100.0	231	1	SOML_PAROL
30	23	100.0	231	1	SOML_SCIOC
31	23	100.0	231	1	SOML_SIGGU
32	23	100.0	232	1	SOML_ACITR
33	23	100.0	232	1	SOML_PROAN
			233	1	SOML_ONCKE
			233	1	P24405 oncorhynch

34	23	100.0	235	1	SOML_GADMO
35	23	100.0	236	1	Y608_PIRAB
36	23	100.0	236	1	YF52_PIRHO
37	23	100.0	237	1	Y450_MYCPN
38	23	100.0	238	1	DSBC_ERWCH
39	23	100.0	245	1	YQJ8_YEAST
40	23	100.0	246	1	NCAP_SFVS
41	23	100.0	261	1	TRMB_XANAC
42	23	100.0	263	1	1439_ARATH
43	23	100.0	266	1	10D2_FUNHE
44	23	100.0	271	1	YDHO_ECOLI
45	23	100.0	277	1	TNR4_HUMAN
46	23	100.0	283	1	PORI_CABEL
47	23	100.0	283	1	Y43C_MYCPN
48	23	100.0	292	1	RBSB_HABIN
49	23	100.0	298	1	CC28_YEAST
50	23	100.0	298	1	ERA_RALSO
51	23	100.0	303	1	V212_FOWPV
52	23	100.0	305	1	E2BA_CABEL
53	23	100.0	318	1	SYGA_MORCA
54	23	100.0	319	1	CNC7_HUMAN
55	23	100.0	319	1	CNC7_MOUSE
56	23	100.0	331	1	SYFA_XANAC
57	23	100.0	332	1	LDHB_ANGRO
58	23	100.0	332	1	LDHD_LACDE
59	23	100.0	343	1	NAGZ_YERPE
60	23	100.0	344	1	SFR6_HUMAN
61	23	100.0	345	1	D2D2_XENLA
62	23	100.0	345	1	KR1_SVUD
63	23	100.0	360	1	LPXB_HELPJ
64	23	100.0	360	1	LPXB_HELPY
65	23	100.0	361	1	PDAG_ARATH
66	23	100.0	366	1	YQCC_BACSU
67	23	100.0	370	1	LEU3_BRAJA
68	23	100.0	375	1	SR55_DROME
69	23	100.0	383	1	TGT_RALSO
70	23	100.0	389	1	BIOF_BACSU
71	23	100.0	389	1	VMSA_HBEVJ
72	23	100.0	390	1	TRA6_ENTFA
73	23	100.0	390	1	TRA6_STAAU
74	23	100.0	420	1	MTCL_HERAU
75	23	100.0	421	1	PHFL_DESVO
76	23	100.0	424	1	BCHN_RHOCA
77	23	100.0	425	1	VRK1_BRARE
78	23	100.0	428	1	HISX_BACTN
79	23	100.0	428	1	HISX_CAMJE
80	23	100.0	428	1	MTBA_BACAR
81	23	100.0	429	1	UTMP_SHEEP
82	23	100.0	431	1	HISX_VIBCH
83	23	100.0	431	1	HISX_VIBPA
84	23	100.0	431	1	HISX_VIBVU
85	23	100.0	437	1	ARLY_CLOAB
86	23	100.0	438	1	ARLY_CLOTE
87	23	100.0	438	1	HISX_SHEON
88	23	100.0	440	1	VRK1_MOUSE
89	23	100.0	442	1	D2D1_XENLA
90	23	100.0	445	1	ADIC_ECO57
91	23	100.0	445	1	ADIC_ECOL6
92	23	100.0	445	1	ADIC_ECOLI
93	23	100.0	445	1	ADIC_SALTY
94	23	100.0	445	1	ADIC_SALTY
95	23	100.0	445	1	ADIC_SHIFL
96	23	100.0	449	1	SCRC_RAT
97	23	100.0	456	1	YMJ5_CABEL
98	23	100.0	466	1	GID_BRUME
99	23	100.0	466	1	HISX_ARATH
100	23	100.0	469	1	HISX_BRAOC
101	23	100.0	470	1	IE63_HSVBB
102	23	100.0	470	1	IE63_HSVBK
103	23	100.0	472	1	GID_RHILLO
104	23	100.0	472	1	GID_RHIME
105	23	100.0	473	1	GARI_HUMAN
106	23	100.0	474	1	GARI_MOUSE

P21919	gadus morhu
Q9V121	pyrococcus
Q92220	pyrococcus
P75127	mycoplasma
P39691	erwinia chr
P53146	saccharomyc
P21793	sandfly fev
Q8Hf4	xanthomonas
Q96299	arabidopsis
P79747	fundulus he
P76190	escherichia
P43489	homo sapien
Q21752	caenorhabdi
P43489	homo sapien
P51513	mycoplasma
P44737	haemophilus
P00546	saccharomyc
Q9Y010	raistonia s
Q9Y523	fowlpox vir
P34604	caenorhabdi
P7892	moraxella c
Q8tb37	homo sapien
Q9cwb8	mus musculu
Q9pj4	xanthomonas
Q9Ygl2	anguilla ro
P26297	lactobacill
Q8zf63	yersinia pe
Q13247	homo sapien
P34973	xenopus lae
Q04543	simian vari
Q25537	helicobacte
Q22263	arabidopsis
P45938	bacillus su
Q89x19	bradyrhizob
P26686	drosophila
Q8xvw4	raistonia s
P5556	bacillus su
P17398	hepatitis b
P59787	enterococc
P1775	staphylococ
P25263	herpetosiph
P13629	desulfovibr
P26164	rhodobacter
Q72u81	brachydanio
Q8ab9	bacteroides
Q9pm77	campylobact
P21814	ovis aries
Q9f854	vibrio chol
Q87q11	vibrio para
Q8d8q0	vibrio vuln
P97k65	clostridium
P59616	clostridium
Q8ef11	shewanella
Q80x41	mus musculu
P24628	xenopus lae
P60063	escherichia
P60062	escherichia
P60061	escherichia
P60065	salmonella
P60066	salmonella
P60064	shigella fl
P23811	rattus norv
P34481	caenorhabdi
Q8ygt4	bruceella me
Q9c5u8	arabidopsis
P24236	brassica ol
P28939	equine herp
Q9506	equine herp
Q98161	rhizobium l
Q92q15	rhizobium m
P24046	homo sapien
P56475	mus musculu

107	23	100.0	474	1	GAR1_RAT	P50572	rattus norv	180	23	100.0	949	1	EMI3_HUMAN	Q9816	homo sapien
108	23	100.0	477	1	SVC_RHIL0	O984x8	rhizobium 1	181	23	100.0	954	1	GCSP_AGR15	Q8ufd6	agrobacteri
109	23	100.0	481	1	ARLY_METMP	O74026	methanococ	182	23	100.0	966	1	CAP1_MESCR	P10490	mesembryant
110	23	100.0	481	1	GID_AGR15	Q8uet6	agrobacteri	183	23	100.0	1002	1	RBMC_MOUSE	P844x3	mus musculus
111	23	100.0	485	1	ANGT_HUMAN	P01019	homo sapien	184	23	100.0	1025	1	LCAP_RAT	P97629	r leucyl-cy
112	23	100.0	485	1	ANGT_PANTR	Q9qln8	pan troglod	185	23	100.0	1027	1	EB30_CABEL	P34441	caenorhabdi
113	23	100.0	485	1	CALB_CAUCR	Q94777	caulobacter	186	23	100.0	1046	1	RPOC_WEIHE	P96177	weissella h
114	23	100.0	489	1	SPR4_MOUSE	Q8ve97	mus musculus	187	23	100.0	1054	1	RPOC_WEIPA	P96178	weissella p
115	23	100.0	490	1	VGLY_LASSG	P17332	lassa virus	188	23	100.0	1129	1	UBPL_SCHPO	Q9utt1	schizosacch
116	23	100.0	491	1	VGLY_LASSU	P08669	lassa virus	189	23	100.0	1134	1	YML7_YEAST	Q03735	saccharomyc
117	23	100.0	494	1	PSD3_DROME	P25161	drosophila	190	23	100.0	1257	1	PER2_MOUSE	O54943	mus musculus
118	23	100.0	494	1	SRF4_HUMAN	Q08170	homo sapien	191	23	100.0	1583	1	GCC2_HUMAN	Q81wj2	homo sapien
119	23	100.0	497	1	RPN3_SCHPO	O42897	schizosacch	192	23	100.0	1607	1	MIPT_LYMET	Q25410	lynnaea sca
120	23	100.0	498	1	GTA_NPVOP	O10302	orygia pseu	193	23	100.0	1778	1	NI89_SCHPO	P47024	saccharomyc
121	23	100.0	498	1	YDHF_SCHPO	Q92360	schizosacch	194	23	100.0	1803	1	YUL3_YEAST	Q94tk4	schizosacch
122	23	100.0	503	1	VRK2_MOUSE	Q8bn21	mus musculus	195	23	100.0	1967	1	CHDA_HUMAN	P952d1	homo sapien
123	23	100.0	508	1	VRK2_HUMAN	Q86y07	homo sapien	196	23	100.0	2095	1	RP1_MOUSE	P56716	mus musculus
124	23	100.0	510	1	MVIN_HAEIN	P44958	haemophilus	197	23	100.0	2156	1	RP1_HUMAN	P56715	homo sapien
125	23	100.0	520	1	TUL2_HUMAN	O00295	homo sapien	198	23	100.0	2215	1	SORL_MOUSE	O88307	m sorillin-
126	23	100.0	534	1	EHD1_HUMAN	Q9h4m9	homo sapien	199	23	100.0	2230	1	GOA4_HUMAN	Q13439	homo sapien
127	23	100.0	534	1	EHD1_MOUSE	Q9vkv4	mus musculus	200	23	100.0	2670	1	IP3T_RAT	Q63269	rattus norv
128	23	100.0	535	1	EHD3_MOUSE	Q9qxy6	mus musculus	201	23	100.0	2671	1	IP3T_HUMAN	Q14573	homo sapien
129	23	100.0	535	1	EHD3_MOUSE	P40412	avena sativ	202	23	100.0	3079	1	IRA2_YEAST	P19158	saccharomyc
130	23	100.0	541	1	EHD4_HUMAN	Q9h223	homo sapien	203	23	100.0	3084	1	MLL2_HUMAN	P19137	mus musculus
131	23	100.0	541	1	EHD4_MOUSE	Q9egp2	mus musculus	204	23	100.0	5262	1	MLL2_HUMAN	O14686	homo sapien
132	23	100.0	543	1	EHD2_HUMAN	Q9hzn4	homo sapien	205	23	100.0	5327	1	MACF_MOUSE	Q9qxd0	mus musculus
133	23	100.0	546	1	EHD3_HUMAN	Q9hzn3	homo sapien	206	23	100.0	5430	1	MACF_HUMAN	Q9upn3	homo sapien
134	23	100.0	558	1	BCHD_EHOSH	O34845	rhodobacter	207	23	100.0	5938	1	MAC4_HUMAN	Q96pk2	homo sapien
135	23	100.0	562	1	TRZM_PANAY	Q47861	pantosea 999	208	23	100.0	8797	1	SNE1_HUMAN	Q8af91	homo sapien
136	23	100.0	595	1	YB85_SCHPO	O14301	schizosacch	209	20	87.0	88	1	S108_MOUSE	P27005	mus musculus
137	23	100.0	605	1	CORO_CABEL	Q21624	caenorhabdi	210	20	87.0	88	1	S108_RAT	P50115	rattus norv
138	23	100.0	609	1	ALBU_HUMAN	P02768	homo sapien	211	20	87.0	104	1	PRTN_PSEAE	Q06552	pseudomonas
139	23	100.0	620	1	YMZ0_YEAST	Q03162	saccharomyc	212	20	87.0	106	1	Y0B5_MYCLE	Q49723	mycobacteri
140	23	100.0	625	1	THIC_XANCP	Q8ph13	xanthomonas	213	20	87.0	119	1	CADC_LISIN	P94887	listeria in
141	23	100.0	625	1	THIC_XANCP	Q8p519	xanthomonas	214	20	87.0	119	1	MP2_NERDI	P80255	nerreis dive
142	23	100.0	638	1	DNAK_BACTN	Q89yw6	bacteroides	215	20	87.0	120	1	HEMM_THERSI	Q99y29	thermozon
143	23	100.0	638	1	DNAK_PRELO	Q93gfl	prevotella	216	20	87.0	124	1	KABI_OLDAP	P56254	oldenlandia
144	23	100.0	647	1	KPC1_APLCA	Q16974	aplysia cal	217	20	87.0	128	1	H2A3_CHICK	P35062	gallus gall
145	23	100.0	676	1	HP1_METAC	Q8tj9a	methanosarc	218	20	87.0	128	1	H2A4_CHICK	P02263	gallus gall
146	23	100.0	676	1	HP1_METMA	Q89y28	methanosarc	219	20	87.0	128	1	H2A_CAIMO	P13912	cairina mos
147	23	100.0	685	1	HPA_NITEU	Q82tf3	nitrosomona	220	20	87.0	134	1	PRL_BUFA	P43001	bufo japoni
148	23	100.0	695	1	PARC_CAUCR	O54479	caulobacter	221	20	87.0	137	1	NUSB_HAEDU	Q7vnd2	haemophilus
149	23	100.0	702	1	LONH_HALNI	Q9hac3	halobacteri	222	20	87.0	138	1	NUSB_BUCAP	Q8K9a2	buchnera ap
150	23	100.0	702	1	YC9Y_ECOLI	P75864	escherichia	223	20	87.0	138	1	NUSB_PHOLL	Q7n0j0	photorhabd
151	23	100.0	706	1	HPA_BRAJA	Q89k83	bradyrhizob	224	20	87.0	138	1	NUSB_YERPE	Q8z442	yersinia pe
152	23	100.0	711	1	CATE_PSERU	P95539	pseudomonas	225	20	87.0	139	1	NUSB_ECOLI	P04381	escherichia
153	23	100.0	711	1	HPA_THETN	Q8rcx1	thermonaer	226	20	87.0	139	1	NUSB_SALTI	Q82x6	salmonella
154	23	100.0	726	1	RNR_BUCAP	Q8K917	buchnera ap	227	20	87.0	139	1	NUSB_SALTY	Q8zrd3	salmonella
155	23	100.0	731	1	BAF1_YEAST	P14164	saccharomyc	228	20	87.0	139	1	RS12_DROME	P80455	drosophila
156	23	100.0	731	1	RNR_BUCAI	P57628	buchnera ap	229	20	87.0	143	1	NUSB_BUCAI	P57535	buchnera ap
157	23	100.0	743	1	STB5_YEAST	P38699	saccharomyc	230	20	87.0	144	1	COPE_MOUSE	P59452	buchnera ap
158	23	100.0	745	1	HG12_ARATH	P46607	arabidopsis	231	20	87.0	144	1	NUSB_BUCBP	P57868	pasteurella
159	23	100.0	753	1	CATE_ECOLI	P21179	escherichia	232	20	87.0	144	1	NUSB_PASMU	Q82z34	caenorhabdi
160	23	100.0	759	1	GLQ2_ARATH	Q9sz11	arabidopsis	233	20	87.0	144	1	PHNO_ECOLI	P16691	escherichia
161	23	100.0	766	1	GLQ1_ARATH	Q9fj62	arabidopsis	234	20	87.0	145	1	Y004_TREPA	Q83050	treponema p
162	23	100.0	788	1	AD07_MOUSE	O35227	mus musculus	235	20	87.0	145	1	Y060_CABEL	O22634	caenorhabdi
163	23	100.0	789	1	AD07_RAT	Q63180	rattus norv	236	20	87.0	155	1	NUSB_VIBFI	Q89g93	vibrio fisc
164	23	100.0	791	1	Y046_UREPA	Q9pr99	ureaplasma	237	20	87.0	155	1	NUSB_VIBPA	Q87ru3	vibrio para
165	23	100.0	799	1	SYFB_CAUCR	Q9a9e5	caulobacter	238	20	87.0	155	1	NUSB_VIBVU	Q8dfa0	vibrio vuln
166	23	100.0	813	1	RNR_ECOLI	P21499	escherichia	239	20	87.0	155	1	NUSB_VIBVY	Q9Kpu5	vibrio chol
167	23	100.0	813	1	RNR_SHIFL	P30851	shigella fl	240	20	87.0	156	1	NUSB_VIBCH	Q9rxs6	deinococcus
168	23	100.0	814	1	KEX2_YEAST	P13134	saccharomyc	241	20	87.0	161	1	ISPF_DEIRA	P82186	mytilus edu
169	23	100.0	821	1	RNR_VIBCH	Q9kny1	vibrio chol	242	20	87.0	181	1	GUN_MYTED	Q82966	yersinia pe
170	23	100.0	825	1	SWI3_YEAST	P32591	saccharomyc	243	20	87.0	192	1	TRPG_YERPE	P29234	mustela vis
171	23	100.0	831	1	PRLR_CHICK	Q04594	gallus gall	244	20	87.0	193	1	PRL_MUSVI	P29234	mustela vis
172	23	100.0	835	1	RNR_VIBPA	P40611	vibrio para	245	20	87.0	196	1	AMIE_PSEAE	P10932	pseudomonas
173	23	100.0	865	1	AC02_ECOLI	P36683	escherichia	246	20	87.0	196	1	R1SE_HALNI	Q9hsl2	halobacteri
174	23	100.0	871	1	IF2_CAMJE	Q9piz1	campylobact	247	20	87.0	198	1	PRL_CHEMY	P33090	chelonina my
175	23	100.0	876	1	TOPI_VIBCH	Q9krb2	vibrio chol	248	20	87.0	199	1	PRL1_ALLMI	P55751	alligator m
176	23	100.0	883	1	RPOL_BPT7	P00573	bacterioph	249	20	87.0	199	1	PRL1_CRONO	P55753	crocodylus
177	23	100.0	884	1	RPOL_BPT3	P07659	bacterioph	250	20	87.0	199	1	PRL2_ALLMI	P55752	alligator m
178	23	100.0	898	1	UBPE_DROME	Q24574	drosophila	251	20	87.0	199	1	PRL2_CRONO	P55754	crocodylus
179	23	100.0	906	1	RPOL_BPK11	P18147	bacterioph	252	20	87.0	199	1	PRL_BALBO	P33089	balaeonopter



253	1	PRL_CAMDR	199	87.0	20	P22393 camelus dro	326	20	87.0	270	1	DLHH_SALTY	Q916m9 salmonella
254	1	PRL_HORSE	199	87.0	20	P12420 equus cabal	327	20	87.0	270	1	SPR5_MOUSE	Q53326 mus musculus
255	1	PRL_LOXAF	199	87.0	20	P10765 loxodonta a	328	20	87.0	271	1	ATFI_HUMAN	P18846 homo sapien
256	1	PS22_ARATH	199	87.0	20	O24633 arabidopsis	329	20	87.0	272	1	SPR5_HUMAN	Q13243 homo sapien
257	1	PRL2_OREMO	200	87.0	20	P09318 oreochromis	330	20	87.0	280	1	EPHB_RHOG	Q47230 r cis-2,3-d
258	1	PRL21_ARATH	204	87.0	20	O23714 arabidopsis	331	20	87.0	287	1	EUTC_PRESM	Q889m3 pseudomonas
259	1	PSB2_TRYBB	206	87.0	20	Q9nbc6 trypanosoma	332	20	87.0	292	1	Y125_MYCTU	Q50608 mycobacteri
260	1	PRL_HYPMO	207	87.0	20	P35395 hypophthalm	333	20	87.0	296	1	ERA_CLOAB	Q97j15 clostridium
261	1	YL95_RALSO	207	87.0	20	P58634 ralstonia s	334	20	87.0	298	1	PANB_BRAJA	Q9ams0 bradyrhizob
262	1	PRL_ANGAN	209	87.0	20	P33096 anguilla an	335	20	87.0	300	1	HAP2_KLUTA	P53768 kluyveromyc
263	1	FLPA_HALN1	210	87.0	20	Q9nqg3 halobacteri	336	20	87.0	300	1	P25055 vaccinia vi	P25055 vaccinia vi
264	1	PRL2_ONCKE	210	87.0	20	P09584 oncorhynch	337	20	87.0	300	1	KRB1_VACCV	P16913 vaccinia vi
265	1	PRL2_ONCKS	210	87.0	20	Q91364 oncorhynch	338	20	87.0	300	1	KRB1_VARV	P33800 varioia vir
266	1	PRL_CARAU	210	87.0	20	P74955 garassius a	339	20	87.0	302	1	YIAL_PSESS	P18205 pseudomonas
267	1	PRL_CORAU	210	87.0	20	P34181 coregonus a	340	20	87.0	303	1	YN37_ARCFU	O27947 archaeoglob
268	1	PRL_CYPCA	210	87.0	20	P09585 cyprinus ca	341	20	87.0	304	1	YR06_CABEL	Q94243 caenorhabdi
269	1	PRL_HYPNO	210	87.0	20	P29235 hypophthalm	342	20	87.0	307	1	COPE_BOVIN	Q28104 bos taurus
270	1	PRL_ONCMY	210	87.0	20	P21993 oncorhynch	343	20	87.0	307	1	COPE_CRIGR	Q60445 cricetus
271	1	PRL_SALSA	211	87.0	20	P48096 salmo salar	344	20	87.0	307	1	COPE_HUMAN	O14579 homo sapien
272	1	PRL1_ONCKE	211	87.0	20	P09583 oncorhynch	345	20	87.0	308	1	ILVE_ECOLI	P00510 escherichia
273	1	PRL_PAROL	211	87.0	20	Q9ygv6 paralichthy	346	20	87.0	308	1	ILVE_SALTY	P15168 salmonella
274	1	PRL1_OREMO	212	87.0	20	P08319 oreochromis	347	20	87.0	309	1	CYP9_CABEL	Q09637 caenorhabdi
275	1	PRL2_DICLA	212	87.0	20	P48249 dicentrarch	348	20	87.0	311	1	CYSM_BACSU	Q34476 bacillus su
276	1	PRL1_ICTFU	212	87.0	20	P51904 ictalurus p	349	20	87.0	313	1	PIP_XANCI	P52279 xanthomonas
277	1	PRL_SPAAR	212	87.0	20	Q93337 sparus aura	350	20	87.0	315	1	FLIM_BUCAI	P57182 buchnera ap
278	1	PSB2_ORYSA	212	87.0	20	Q91st6 oryza sativ	351	20	87.0	317	1	CC28_CANAL	P43063 candida alb
279	1	RPSD_MYCTU	212	87.0	20	Q50712 mycobacteri	352	20	87.0	317	1	YMT8_YEAST	O44659 saccharomyc
280	1	GPH_RHOSH	218	87.0	20	P35650 rhodobacter	353	20	87.0	319	1	PLSX_CHLMO	Q9p1b1 chlamydia m
281	1	MAD_HUMAN	221	87.0	20	Q05195 homo sapien	354	20	87.0	321	1	PLSX_CHLTR	O48177 chlamydia t
282	1	FFP_BACSU	224	87.0	20	Q9f4f7 bacillus su	355	20	87.0	323	1	RLAO_LELIN	P39097 leishmania
283	1	LP14_BACSU	224	87.0	20	P39144 bacillus su	356	20	87.0	331	1	YB94_METTH	O27262 methanobact
284	1	SFP_BACSU	224	87.0	20	P39135 bacillus su	357	20	87.0	332	1	CREM_HUMAN	Q03060 homo sapien
285	1	PRL_MESAU	226	87.0	20	P37884 mesocricetu	358	20	87.0	336	1	DUSA_PSEPK	Q88kx0 pseudomonas
286	1	PRL_MOUSE	226	87.0	20	P06879 mus musculu	359	20	87.0	336	1	LEGC_HUMAN	Q96d00 homo sapien
287	1	PRL_RAT	226	87.0	20	P01237 rattus norv	360	20	87.0	338	1	GPDA_STRPN	Q97nf1 streptococc
288	1	GPH_RHILO	227	87.0	20	Q98m18 rhizobium l	361	20	87.0	338	1	GPDA_STRPN	Q8dn59 streptococc
289	1	PRL_HUMAN	227	87.0	20	P01236 homo sapien	362	20	87.0	341	1	CREM_MOUSE	P27699 mus musculu
290	1	PRL_MACMU	227	87.0	20	P55151 macaca mula	363	20	87.0	341	1	CREM_RAT	Q03061 rattus norv
291	1	PRL_RABIT	227	87.0	20	Q28632 oryctolagus	364	20	87.0	341	1	NAGZ_ECO57	P58067 escherichia
292	1	PRL_MONDO	228	87.0	20	O62819 monodelphis	365	20	87.0	341	1	NAGZ_ECOL6	Q8fin2 escherichia
293	1	PRL_TRIVU	228	87.0	20	O62781 trichosurus	366	20	87.0	341	1	NAGZ_ECOLI	P75949 escherichia
294	1	SOML_ANGAN	228	87.0	20	Q90216 anguilla an	367	20	87.0	341	1	NAGZ_SALTI	Q8zq06 salmonella
295	1	PRL_CHICK	229	87.0	20	P14676 gallus gall	368	20	87.0	341	1	NAGZ_SALTY	O8zq06 salmonella
296	1	PRL_FELCA	229	87.0	20	P46403 felis silve	369	20	87.0	344	1	CREM_CANFA	P79145 canis fami
297	1	PRL_MELGA	229	87.0	20	P17572 meleagris g	370	20	87.0	344	1	VPO_EPP2	P25480 bacterioph
298	1	PRL_EIG	229	87.0	20	P01238 sus scrofa	371	20	87.0	344	1	Y496_MYCTU	Q11161 mycobacteri
299	1	YC22_ARATH	232	87.0	20	O81916 arabidopsis	372	20	87.0	345	1	DHAS_MYCTU	P37049 mycobacteri
300	1	PYRH_MYCPN	235	87.0	20	P75165 mycoplasma	373	20	87.0	348	1	TRPD_CORGL	P06559 corynebacte
301	1	Y141_METTH	236	87.0	20	O26244 methanobact	374	20	87.0	349	1	ESR1_ANOCA	Q9yht3 anolis caro
302	1	OPAJ_NEIGO	237	87.0	20	Q04882 neisseria g	375	20	87.0	351	1	CBF1_YEAST	P17106 saccharomyc
303	1	OPAK_NEIGO	237	87.0	20	Q04880 neisseria g	376	20	87.0	351	1	HSF3_LYCPE	P41132 lycopersico
304	1	YG02_METKA	237	87.0	20	Q8tu29 methanopyru	377	20	87.0	356	1	IRXH_CABEL	Q93348 caenorhabdi
305	1	HS6A_DRONE	238	87.0	20	P05812 drosophila	378	20	87.0	357	1	HRCU_RALSO	P35652 ralstonia s
306	1	RESB_BACSU	240	87.0	20	P35163 bacillus su	379	20	87.0	358	1	V044_FOWPV	Q9j5f9 fowlpox vir
307	1	FKBY_HABIN	241	87.0	20	P44760 haemophilus	380	20	87.0	358	1	Y502_MYCTU	Q11167 mycobacteri
308	1	YE88_SCHPO	241	87.0	20	O14304 schizosacch	381	20	87.0	361	1	AROB_MYCLE	Q9ccs4 mycobacteri
309	1	YH77_ARCFU	245	87.0	20	O28497 archaeoglob	382	20	87.0	361	1	IE63_PVKA	Q85232 pseudorabie
310	1	YSE0_STRCO	250	87.0	20	Q9zbn3 streptomyce	383	20	87.0	362	1	AROB_MYCTU	P36919 mycobacteri
311	1	Y264_STRAU	251	87.0	20	Q9x4h5 streptomyce	384	20	87.0	363	1	ATZD_PSESD	P58329 pseudomonas
312	1	YDA6_SCHPO	252	87.0	20	Q10348 schizosacch	385	20	87.0	363	1	CYA2_RHIME	Q52915 rhizobium m
313	1	MODA_HABIN	254	87.0	20	P45323 haemophilus	386	20	87.0	364	1	P16P_XANFL	P23014 xanthobacte
314	1	NCAP_UUK	254	87.0	20	P22025 uukuniemi v	387	20	87.0	365	1	SRP2_SCHPO	P78814 schizosacch
315	1	GLO2_RHOB	255	87.0	20	P05446 rhodopsu	388	20	87.0	367	1	Y502_MYCLB	P54878 mycobacteri
316	1	MTNA_MYCTU	255	87.0	20	Q10889 mycobacteri	389	20	87.0	375	1	PER_DROCP	P91607 drosophila
317	1	GLO2_RHOCA	256	87.0	20	P96981 rhodobacter	390	20	87.0	380	1	YH07_PASMU	Q9ckb7 pasteurella
318	1	MODA_ECOLI	257	87.0	20	P73329 escherichia	391	20	87.0	382	1	ACBC_ACTS5	Q9zae9 actinoplan
319	1	NADC_ARCFU	258	87.0	20	O28439 archaeoglob	392	20	87.0	382	1	ISDF_CAUCR	Q9a715 c ispd/ispf
320	1	DPHB_METTH	264	87.0	20	O27902 methanobact	393	20	87.0	396	1	INTB_ECOLI	P39347 escherichia
321	1	SUE1_PYRAE	266	87.0	20	Q8zu79 pyrobaculum	394	20	87.0	398	1	KBL_ECOLI	P07912 escherichia
322	1	STO3_CABEL	267	87.0	20	Q20657 caenorhabdi	395	20	87.0	398	1	KBL_SALTY	P37419 salmonella
323	1	ATFI_MOUSE	269	87.0	20	P81269 mus musculu	396	20	87.0	400	1	ASSY_SYNY3	P77973 synecocyst
324	1	SPR5_RAT	269	87.0	20	Q99167 rattus norv	397	20	87.0	400	1	ISDF_AGR5	O8uff4 a ispd/ispf
325	1	DLHH_SALTI	270	87.0	20	Q8z3b8 salmonella	398	20	87.0	401	1	ASSY_SYNEL	Q8dky7 synecococc

399	20	87.0	402	1	CPXF_STRGO	P18327 streptomyce	472	20	87.0	538	1	IF3C_EUGGR	P36177 euglena gra
400	20	87.0	402	1	VZ2_HPV65	Q07851 human papil	473	20	87.0	547	1	YJDB_ECOLI	P30845 escherichia
401	20	87.0	403	1	MTB1_BREPE	P10283 brevbacter	474	20	87.0	547	1	YJDB_SALTY	P36555 salmonella
402	20	87.0	404	1	MTB1_ECOLI	P10283 brevbacter	475	20	87.0	557	1	ILVD_NIFEU	Q82xv7 nitrosomona
403	20	87.0	406	1	FABB_ECOLI	P14926 escherichia	476	20	87.0	560	1	ILVD_SYNLE	Q84k13 synecococc
404	20	87.0	408	1	DEOB_BUCBP	Q89a57 buchnera ap	477	20	87.0	573	1	301D_COMTE	Q06401 comamonas t
405	20	87.0	409	1	MFGM_PIG	P79385 sus scrofa	478	20	87.0	575	1	NRD1_YEAST	P33617 saccharomyc
406	20	87.0	411	1	R227_HUMAN	Q92552 homo sapien	479	20	87.0	575	1	RECJ_ERWCH	P33693 erwinia chr
407	20	87.0	415	1	PIC1_HUMAN	Q9nrd5 homo sapien	480	20	87.0	577	1	MTG8_MOUSE	Q61909 mus musculu
408	20	87.0	416	1	PIC1_MOUSE	Q62083 mus musculu	481	20	87.0	578	1	MM17_MOUSE	Q91083 mus musculu
409	20	87.0	416	1	PIC1_RAT	Q9ep80 rattus norv	482	20	87.0	579	1	ESR1_SPAAU	Q9pyv9 sparus auro
410	20	87.0	416	1	THAA_HPPI	Q91241 paralichthy	483	20	87.0	581	1	ESR1_PAGMA	P07362 pagrus mayo
411	20	87.0	416	1	THAA_HPPI	Q91241 paralichthy	484	20	87.0	581	1	PRIM_SALTY	O43132 salmonella
412	20	87.0	422	1	KXSL_STRCN	Q02578 streptomyce	485	20	87.0	583	1	ESR1_ORENI	P50240 oreochromis
413	20	87.0	424	1	MS1L_ARATH	O22467 arabidopsis	486	20	87.0	585	1	ESR1_ORENI	Q9yh33 oreochromis
414	20	87.0	431	1	NRKB_TRYBB	Q08942 trypanosoma	487	20	87.0	586	1	ESR1_XENLA	P81559 xenopus lae
415	20	87.0	431	1	NRKB_TRYBB	Q03428 trypanosoma	488	20	87.0	587	1	ESR1_POEUG	Q91250 poephila gu
416	20	87.0	438	1	AMV1_HORVU	P00693 hordeum vul	489	20	87.0	589	1	ESR1_CHICK	Q91212 gallus gall
417	20	87.0	440	1	SCRC_HUMAN	P47872 homo sapien	490	20	87.0	590	1	YMW7_YEAST	P33863 saccharomyc
418	20	87.0	442	1	MNTH_RALSO	Q8xsf6 ralstonia s	491	20	87.0	592	1	YKO6_CAEEL	P34294 caenorhabdi
419	20	87.0	443	1	AM2A_ORYSA	P27935 oryza sativ	492	20	87.0	594	1	ESR1_HORSE	Q9tv98 equus cabal
420	20	87.0	445	1	AMC2_ORYSA	P27941 oryza sativ	493	20	87.0	595	1	ESR1_HUMAN	P03372 homo sapien
421	20	87.0	445	1	SCRC_RABIT	O46502 oryctolagus	494	20	87.0	595	1	ESR1_MESAU	Q94zj5 mesocricetu
422	20	87.0	448	1	GC5A_BACSU	P54376 bacillus su	495	20	87.0	595	1	ESR1_PIG	Q23040 sus scrofa
423	20	87.0	448	1	YG4Q_YEAST	P50079 saccharomyc	496	20	87.0	599	1	ESR1_MOUSE	P13785 mus musculu
424	20	87.0	451	1	BPPE_BACSU	P32959 bacillus su	497	20	87.0	600	1	ESR1_RAT	P06211 rattus norv
425	20	87.0	463	1	ARLY_CHLTE	Q8xdj5 chlorobium	498	20	87.0	601	1	NCPR_SALTR	P13618 salmo trutt
426	20	87.0	466	1	UXAC_BRUME	Q8ycq2 brucella me	499	20	87.0	604	1	MTG8_HUMAN	Q06455 homo sapien
427	20	87.0	466	1	UXAC_BRUSU	Q8fvm4 brucella su	500	20	87.0	606	1	WDR1_HUMAN	Q75083 homo sapien
428	20	87.0	469	1	UXAC_RHILO	Q98ew1 rhizobium l	501	20	87.0	606	1	WDR1_MOUSE	O89342 mus musculu
429	20	87.0	469	1	UXAC_RHIME	Q92v04 rhizobium m	502	20	87.0	608	1	WDR1_CHICK	Q93277 gallus gall
430	20	87.0	471	1	MURD_STRCO	Q9s2w9 streptomyce	503	20	87.0	609	1	WDR1_MOUSE	Q93277 gallus gall
431	20	87.0	479	1	CATA_DESYM	Q92n99 desulfovibr	504	20	87.0	614	1	MGM_EUBBA	Q53268 eubacterium
432	20	87.0	479	1	CATA_PSEPU	Q53714 pseudomonas	505	20	87.0	619	1	ESR1_ICTPU	Q9yhz7 ictalurus p
433	20	87.0	480	1	RADA_MYCTU	O53570 mycobacteri	506	20	87.0	617	1	ESR1_ORYLA	P52410 oryzias lat
434	20	87.0	482	1	CATA_BACSU	P26901 bacillus su	507	20	87.0	620	1	ESR1_ORYLA	P21910 xenopus lae
435	20	87.0	482	1	CATA_ONCVE	Q27710 onchocerca	508	20	87.0	623	1	LM2_XENLA	Q9nhd2 halobacteri
436	20	87.0	482	1	CATA_PSEAL	O52762 pseudomonas	509	20	87.0	631	1	SVR_HALNI	Q89a36 buchnera ap
437	20	87.0	483	1	BCA_STRVL	P33569 streptomyce	510	20	87.0	640	1	PTMA_BUCBP	Q8k911 buchnera ap
438	20	87.0	484	1	CATA_PROMI	P42321 proteus mir	511	20	87.0	649	1	PTMA_BUCAP	Q08032 saccharomyc
439	20	87.0	485	1	YB47_MYCPN	P75139 mycoplasma	512	20	87.0	650	1	CC45_YEAST	Q09166 homo sapien
440	20	87.0	487	1	CATA_STRCO	Q94598 streptomyce	513	20	87.0	663	1	PD11_HUMAN	P08313 herpes simp
441	20	87.0	489	1	VGLY_MOPEI	P19240 mopeia viru	514	20	87.0	664	1	UL47_HSV1P	P72656 synecocyst
442	20	87.0	492	1	CPAC_MOUSE	P56593 mus musculu	515	20	87.0	674	1	RNE_SYNY3	P16435 homo sapien
443	20	87.0	492	1	MURE_STAAC	O86491 staphylococ	516	20	87.0	676	1	NCPR_HUMAN	P37039 cavia porce
444	20	87.0	494	1	CATA_RHIME	P95631 rhizobium m	517	20	87.0	677	1	NCPR_CAVPO	P37040 mus musculu
445	20	87.0	494	1	CPA6_HUMAN	P11509 homo sapien	518	20	87.0	677	1	NCPR_MOUSE	P04175 sus scrofa
446	20	87.0	494	1	MURE_STAAM	Q99v74 staphylococ	519	20	87.0	677	1	NCPR_RAT	P00388 rattus norv
447	20	87.0	494	1	MURE_STAAM	Q8nxc2 staphylococ	520	20	87.0	677	1	NCPR_RAT	P00389 oryctolagus
448	20	87.0	494	1	MURE_STAEP	Q8cpr2 staphylococ	521	20	87.0	679	1	NCPR_RABIT	Q07093 drosophila
449	20	87.0	498	1	CATA_BRUME	Q59170 brucella me	522	20	87.0	683	1	CYGH_DROME	P54341 bacillus su
450	20	87.0	498	1	CATA_BRUSU	Q8fwu0 brucella su	523	20	87.0	687	1	XKDV_YEAST	P38338 saccharomyc
451	20	87.0	501	1	CP36_RABIT	P11707 oryctolagus	524	20	87.0	688	1	YB9F_YEAST	P94281 bartonella
452	20	87.0	501	1	CP3V_MESAU	O70537 mesocricetu	525	20	87.0	692	1	GYRB_BARBA	P10231 herpes simp
453	20	87.0	503	1	CP33_HUMAN	P51584 homo sapien	526	20	87.0	693	1	UL47_HSV1P	Q9xzc8 schistocerc
454	20	87.0	503	1	CP39_RAT	P01338 rattus norv	527	20	87.0	697	1	SM2A_SCHGR	Q24323 drosophila
455	20	87.0	503	1	NUSA_RICPR	Q9zoz7 rickettsia	528	20	87.0	706	1	SM2A_DROME	P28950 equine herp
456	20	87.0	504	1	CP341_MOUSE	Q9jma7 mus musculu	529	20	87.0	706	1	UL17_HSVIB	P12419 reovirus (t
457	20	87.0	504	1	CP3G_MOUSE	Q64481 mus musculu	530	20	87.0	719	1	VM3_REOVD	Q04564 agrobacteri
458	20	87.0	509	1	P233_HUMAN	Q9n220 homo sapien	531	20	87.0	723	1	TR2M_AGRVI	P49480 odontella s
459	20	87.0	512	1	UGTB_CAEEL	Q22180 caenorhabdi	532	20	87.0	733	1	PSAB_ODOSI	O78507 guillardia
460	20	87.0	514	1	CP23_DROME	Q01520 drosophila	533	20	87.0	734	1	PSAB_GUTH	P51285 porphyra pu
461	20	87.0	514	1	CP24_RAT	Q91228 rattus norv	534	20	87.0	734	1	PSAB_PORPU	O54408 bacillus su
462	20	87.0	514	1	IMD1_MOUSE	P50096 mus musculu	535	20	87.0	735	1	AD02_WACFA	Q28478 macaca fasc
463	20	87.0	515	1	CATA_YEAST	P15202 saccharomyc	536	20	87.0	740	1	ND0L_HUMAN	Q9uqul homo sapien
464	20	87.0	523	1	PUR9_MYCTU	P71553 m bifunctio	537	20	87.0	740	1	TR2M_AGRRH	Q09109 agrobacteri
465	20	87.0	525	1	ESR1_MICUN	P57753 micropogoni	538	20	87.0	749	1	PSAA_CVACA	Q9t1q5 cyanidium c
466	20	87.0	526	1	SRC_RSVH1	P25020 rous sarcom	539	20	87.0	752	1	TR2M_AGRRH	Q10665 caenorhabdi
467	20	87.0	526	1	SRC_RSVH1	P00526 rous sarcom	540	20	87.0	754	1	MES3_CAEEL	P04029 agrobacteri
468	20	87.0	527	1	PUR9_MYCLE	Q925h5 m bifunctio	541	20	87.0	755	1	TR2M_AGRTH	P25017 agrobacteri
469	20	87.0	527	1	PUR9_MYCPA	Q9rajs m bifunctio	542	20	87.0	755	1	TR2N_AGRVI	P39925 saccharomyc
470	20	87.0	527	1	RHGB_ASPAC	Q00019 aspergillus	543	20	87.0	761	1	APG3_AGRVI	P39925 saccharomyc
471	20	87.0	534	1	EK11_YEAST	Q03764 saccharomyc	544	20	87.0	763	1	PEPX_LACLA	Q9c601 lactococcus

545	20	87.0	765	1	TOP1_HUMAN	P11387	homo sapien	618	20	87.0	1235	1	DPOL_HSV1A	P07917	herpes simp
546	20	87.0	767	1	RIR1_HSV8A	Q01037	herpesvirus	619	20	87.0	1235	1	DPOL_HSV1K	P04292	herpes simp
547	20	87.0	767	1	TOP1_CERAE	Q7YR26	cercopithec	620	20	87.0	1235	1	DPOL_HSV1S	P09854	herpes simp
548	20	87.0	767	1	TOP1_CRIGR	Q07050	cricetulus	621	20	87.0	1240	1	DPOL_HSV21	P07918	herpes simp
549	20	87.0	767	1	TOP1_MOUSE	Q04750	mus musculus	622	20	87.0	1300	1	POL2_MOUSE	P11369	mus musculus
550	20	87.0	768	1	DAB2_RAT	O88797	rattus norv	623	20	87.0	1371	1	PUR2_CHITE	Q26255	c.trifuncti
551	20	87.0	770	1	PRTP_VZVD	P09284	varicella-z	624	20	87.0	1428	1	ATRN_MOUSE	Q9WU60	mus musculus
552	20	87.0	772	1	ANNU_SCHAM	P52183	schistocerc	625	20	87.0	1429	1	ATRN_HUMAN	Q95882	homo sapien
553	20	87.0	776	1	YOKS_CAEEL	Q11177	caenorhabdi	626	20	87.0	1454	1	PTPT_MOUSE	Q99M80	mus musculus
554	20	87.0	780	1	PRTP_HSV1F	P06490	herpes simp	627	20	87.0	1463	1	DPO3_STRPN	Q975Q2	streptococc
555	20	87.0	785	1	PRTP_HSV11	P10212	herpes simp	628	20	87.0	1463	1	DPO3_STRER6	O8dra5	streptococc
556	20	87.0	785	1	PRTP_HSV1A	P12835	herpes simp	629	20	87.0	1463	1	PTPT_HUMAN	O14522	homo sapien
557	20	87.0	789	1	PHK_BRUSU	P12835	herpes simp	630	20	87.0	1465	1	DPO3_STRP3	O14522	homo sapien
558	20	87.0	792	1	PHK_BRUME	O8TWRO	brucella su	631	20	87.0	1465	1	DPO3_STRP8	O14522	homo sapien
559	20	87.0	792	1	RECQ_AQUAE	O6YB18	brucella me	632	20	87.0	1465	1	DPO3_STRP8	O14522	homo sapien
560	20	87.0	793	1	RECQ_AQUAE	O6YB18	brucella me	633	20	87.0	1468	1	DPO3_STRP3	O14522	homo sapien
561	20	87.0	795	1	HS2_KLULA	O13471	kluveromyc	634	20	87.0	1538	1	PPSB_MYCTU	O10978	mycobacteri
562	20	87.0	803	1	SW16_YEAST	P09959	saccharomyc	635	20	87.0	1551	1	VGLM_DUGBV	Q20004	dugbe virus
563	20	87.0	809	1	OSTA_XANCP	O8PEO0	xanthomonas	636	20	87.0	1657	1	STNB_CABEL	Q90761	caenorhabdi
564	20	87.0	825	1	ICP0_HSV2H	P28284	herpes simp	637	20	87.0	1739	1	CHD2_HUMAN	O14647	homo sapien
565	20	87.0	829	1	TOP1_XENLA	P41512	xenopus lae	638	20	87.0	1739	1	CHD2_HUMAN	O14647	homo sapien
566	20	87.0	842	1	HS2_PICPA	P43533	pichia past	639	20	87.0	1795	1	ESPI_HUMAN	O14674	homo sapien
567	20	87.0	852	1	WS14_HUMAN	Q9NP71	homo sapien	640	20	87.0	1795	1	LMB2_MOUSE	O61292	mus musculus
568	20	87.0	865	1	MUTS_BACHD	Q9KAC0	bacillus ha	641	20	87.0	1927	1	LPH_HUMAN	P09848	homo sapien
569	20	87.0	865	1	PMJ1_HUMAN	O43490	homo sapien	642	20	87.0	1942	1	HELZ_HUMAN	P42694	homo sapien
570	20	87.0	868	1	TOP1_HAENI	P43012	haemophilus	643	20	87.0	1986	1	WA_EMENI	Q03149	emeritella
571	20	87.0	869	1	DPM1_YEAST	P05374	saccharomyc	644	20	87.0	1997	1	PTPB_HUMAN	P23467	homo sapien
572	20	87.0	880	1	DPM1_BACSU	O34996	bacillus su	645	20	87.0	2032	1	TRPG_CABEL	Q93971	caenorhabdi
573	20	87.0	880	1	YL86_YEAST	O65708	saccharomyc	646	20	87.0	2095	1	RRPL_TOSV	P37800	toscana vir
574	20	87.0	884	1	Y9P7_MYCTU	Q50654	mycobacteri	647	20	87.0	2138	1	SPCB_MOUSE	P15508	mus musculus
575	20	87.0	884	1	Y9P7_MYCTU	P59974	mycobacteri	648	20	87.0	2137	1	SPCB_HUMAN	P11277	homo sapien
576	20	87.0	893	1	XN8R_YEAST	P53739	saccharomyc	649	20	87.0	2359	1	CCAH_RAT	Q9EQ60	rattus norv
577	20	87.0	905	1	CHO2_SCHPO	O74787	schizosacch	650	20	87.0	2365	1	CCAH_MOUSE	O88427	mus musculus
578	20	87.0	911	1	CIAP_BACTU	P96315	bacillus th	651	20	87.0	2483	1	COA2_HUMAN	P00763	homo sapien
579	20	87.0	916	1	SVI_STAEP	O8CXL1	staphylococ	652	20	87.0	2672	1	GCN1_YEAST	P33892	saccharomyc
580	20	87.0	920	1	VGLE_HSVSM	Q04464	herpesvirus	653	20	87.0	3075	1	LMAL_HUMAN	P25391	homo sapien
581	20	87.0	925	1	NFC2_HUMAN	Q13469	homo sapien	654	20	87.0	4427	1	PKSL_BACSU	Q95470	bacillus su
582	20	87.0	926	1	ATCL_SYN7P	P37278	synectococc	655	20	87.0	5120	1	PCLO_CHICK	Q9PU36	gallus gall
583	20	87.0	954	1	DRP2_HUMAN	Q13474	homo sapien	656	19	82.6	48	1	DJBB_CANFA	P19199	canis famil
584	20	87.0	959	1	MLM4_MYLE	P54881	mycobacteri	657	19	82.6	62	1	COXS_HUMAN	O14061	homo sapien
585	20	87.0	968	1	NML2_MYCTU	Q11171	mycobacteri	658	19	82.6	62	1	COXS_MOUSE	P56394	mus musculus
586	20	87.0	970	1	TRAL_COMTE	Q04222	comamonas t	659	19	82.6	62	1	COXS_PIG	P81045	sus scrofa
587	20	87.0	988	1	TNP2_ECOLI	P06694	escherichia	660	19	82.6	63	1	IBB_VICFA	P24661	vicia faba
588	20	87.0	1008	1	SN14_YEAST	P36048	saccharomyc	661	19	82.6	71	1	GRGI_NEUCR	P22151	neurospora
589	20	87.0	1019	1	VP3_RDVA	P22472	rice dwarf	662	19	82.6	72	1	IBB_VICAN	P01065	vicia angus
590	20	87.0	1020	1	VP3_RDVF	Q98630	rice dwarf	663	19	82.6	80	1	DIPA_PROTE	P03715	bacterioph
591	20	87.0	1029	1	Z197_HUMAN	O8NB25	homo sapien	664	19	82.6	82	1	VIOC_BPT4	P10836	protophormi
592	20	87.0	1032	1	TU9_MOUSE	Q9EQU3	mus musculus	665	19	82.6	84	1	SCX4_ANDAU	P45658	androctonus
593	20	87.0	1039	1	VP19_YEAST	Q07468	saccharomyc	666	19	82.6	86	1	DINJ_ECOLI	Q7150	escherichia
594	20	87.0	1052	1	FAK1_HUMAN	Q05397	homo sapien	667	19	82.6	88	1	YB63_SHEON	Q8HQ4	shewanella
595	20	87.0	1055	1	EPB2_HUMAN	P29327	homo sapien	668	19	82.6	89	1	YFU3_BAGST	Q04730	bacillus st
596	20	87.0	1055	1	FAK1_RAT	Q35346	rattus norv	669	19	82.6	91	1	R37A_SCHMA	O17307	schistosoma
597	20	87.0	1060	1	EGS1_XENLA	P28025	xenopus lae	670	19	82.6	92	1	DEFI_DROME	P36192	drosophila
598	20	87.0	1061	1	DPOL_ADE12	P06538	human adeno	671	19	82.6	96	1	IBBA_PEA	Q41065	pisum sativ
599	20	87.0	1062	1	NAL2_HUMAN	Q9NX02	homo sapien	672	19	82.6	100	1	Y050_MYCPU	Q98R19	mycoplasma
600	20	87.0	1064	1	NFC2_MOUSE	O60591	mus musculus	673	19	82.6	101	1	CLPS_CLOAB	Q97131	clostridium
601	20	87.0	1067	1	EGS2_XENLA	Q91783	xenopus lae	674	19	82.6	101	1	DIPD_PROTE	P18684	protophormi
602	20	87.0	1068	1	FAK1_XENLA	Q91738	xenopus lae	675	19	82.6	103	1	VG56_BPML5	Q05266	mycobacteri
603	20	87.0	1070	1	Y355_HUMAN	Q19738	xenopus lae	676	19	82.6	104	1	VILL_ECOLI	P32156	escherichia
604	20	87.0	1075	1	RPOB_WHEAT	Q15063	homo sapien	677	19	82.6	105	1	VG68_BPPH2	P16518	bacterioph
605	20	87.0	1076	1	RPOB_WHEAT	P16023	zea mays (m	678	19	82.6	108	1	GLPE_ECO57	Q9X625	escherichia
606	20	87.0	1090	1	FAK1_MOUSE	Q9XP87	triticum ae	679	19	82.6	108	1	GLPE_ECOLI	P09390	escherichia
607	20	87.0	1107	1	FAK1_MOUSE	P34152	mus musculus	680	19	82.6	110	1	VATF_BOVIN	Q28029	bos taurus
608	20	87.0	1107	1	FAK1_MOUSE	P34152	mus musculus	681	19	82.6	111	1	FLIE_CLOAB	Q97H50	clostridium
609	20	87.0	1122	1	DPOL_ADE07	P05664	human adeno	682	19	82.6	111	1	TBCA_ARATH	Q04350	arabidopsis
610	20	87.0	1155	1	CIAB_BACTK	P06578	bacillus th	683	19	82.6	114	1	IBB2_PEA	Q41066	pisum sativ
611	20	87.0	1159	1	N124_SCHPO	Q09904	schizosacch	684	19	82.6	114	1	MSPJ_SAGOE	Q97949	saginus oe
612	20	87.0	1174	1	NIFJ_ECOLI	P52647	escherichia	685	19	82.6	115	1	Y6F172	P36172	escherichia
613	20	87.0	1178	1	CIAC_BACTK	P05068	bacillus th	686	19	82.6	117	1	YG45_YEAST	P53300	saccharomyc
614	20	87.0	1188	1	DPOL_ADE40	P48311	human adeno	687	19	82.6	119	1	VATF_HUMAN	Q16864	homo sapien
615	20	87.0	1193	1	DPOL_ADE04	P87503	human adeno	688	19	82.6	119	1	VATF_RAT	P50408	rattus norv
616	20	87.0	1194	1	DPOL_VZVD	P09252	varicella-z	689	19	82.6	121	1	GLB_TETPY	P17724	tetrachyena
617	20	87.0	1200	1	MOGS_CAEEL	Q09530	caenorhabdi	690	19	82.6	121	1	GLB_TETPY	P37325	synectocyst
618	20	87.0	1235	1	DPOL_HSV11	P04293	herpes simp	690	19	82.6	124	1	GLBN_SYNY3	Q73925	synectocyst

691	19	82.6	124	1	YABJ_BACSU	P37552	19	82.6	160	1	ISPF_CORGL	Q8nmb9
692	19	82.6	124	1	YOB_A_ECOLI	P76279	19	82.6	160	1	ISPF_FUSNN	Q86e7
693	19	82.6	126	1	MSA_BOREU	P51339	19	82.6	160	1	R73_RICNN	Q82j94
694	19	82.6	127	1	FLIE_LEPIN	O81952	19	82.6	160	1	R73_RICPR	Q82j94
695	19	82.6	129	1	HMWR_RHILV	Q9x5v4	19	82.6	161	1	NAPB_PARP	Q8351
696	19	82.6	129	1	VP14_BPAPS	Q9xtt4	19	82.6	161	1	T2DA_HUMAN	Q81514
697	19	82.6	130	1	YRGK_CAEBL	Q93408	19	82.6	162	1	ISPF_HERPE	Q82bp7
698	19	82.6	139	1	DH1_HORVU	P12951	19	82.6	162	1	RIFK_HUMAN	Q859g6
699	19	82.6	139	1	FOB2_STAPF	Q03377	19	82.6	162	1	CDNA_FELCA	Q15002
700	19	82.6	140	1	ATPE_NEIMA	Q91w69	19	82.6	164	1	T2DA_XENLA	Q81858
701	19	82.6	140	1	ATPE_NEIMA	Q91w69	19	82.6	164	1	T2DA_XENLA	Q81858
702	19	82.6	141	1	NUSB_NEIMA	Q91vd5	19	82.6	165	1	NUSB_PSSSM	Q889q5
703	19	82.6	141	1	NUSB_NEIMA	Q91vd5	19	82.6	165	1	NUSB_PSSSM	Q889q5
704	19	82.6	141	1	YV2_DHV11	Q01480	19	82.6	166	1	LUXS_HAEIN	P44007
705	19	82.6	141	1	ZURR_LISMO	Q91480	19	82.6	166	1	LUXS_HAEIN	P44007
706	19	82.6	142	1	FOB1_STAPF	P52921	19	82.6	166	1	NUSB_PSEPK	Q88qhs
707	19	82.6	143	1	SILE_SALTY	Q944n3	19	82.6	166	1	NUSB_PSEPK	Q88qhs
708	19	82.6	146	1	HBB_ALIMI	P02130	19	82.6	167	1	NUSB_NITRU	Q82807
709	19	82.6	147	1	TPC_TODPA	Q9b1g0	19	82.6	168	1	NRXA_RALSO	Q82xpi
710	19	82.6	147	1	NUSB_CHRVO	O7bvf2	19	82.6	169	1	Y224_METUA	P57677
711	19	82.6	150	1	GLPA_HUMAN	P02724	19	82.6	169	1	YLAC_ECOLI	P77523
712	19	82.6	150	1	YBF2_STRAU	P23714	19	82.6	170	1	DEF2_XANAC	Q89g20
713	19	82.6	151	1	GLBK_CHITH	P02228	19	82.6	170	1	DEF2_XANCP	Q894f9
714	19	82.6	151	1	R13_METKA	Q84vc1	19	82.6	172	1	ADXH_DROME	P37193
715	19	82.6	152	1	DEF_WIGBR	O84258	19	82.6	172	1	ADXH_DROME	P37193
716	19	82.6	152	1	ILFA_MOUSE	Q84258	19	82.6	172	1	ADXH_DROME	P37193
717	19	82.6	152	1	RVXK_BIFLO	O84559	19	82.6	175	1	IF3_THEMA	Q8xw1
718	19	82.6	153	1	IP2K_SOLTU	Q84559	19	82.6	175	1	IF3_THEMA	Q8xw1
719	19	82.6	154	1	IP27_SOLTU	Q98q74	19	82.6	176	1	YV11_CAEBL	Q11088
720	19	82.6	154	1	MRAZ_MYCPU	Q98q74	19	82.6	176	1	YV11_CAEBL	Q11088
721	19	82.6	155	1	IGPF_CLOAB	Q971x0	19	82.6	177	1	HTRC_ECOLI	P27375
722	19	82.6	155	1	RIFK_MOUSE	Q8cfv9	19	82.6	177	1	HTRC_ECOLI	P27375
723	19	82.6	155	1	R73_BACST	P22744	19	82.6	179	1	ORN_VIBVU	Q84cv6
724	19	82.6	155	1	R73_BACSU	P22744	19	82.6	179	1	ORN_VIBVU	Q84cv6
725	19	82.6	155	1	RST_CORGL	Q8nt20	19	82.6	181	1	LGUL_EBRAJU	O44885
726	19	82.6	155	1	RST_HELPI	P50014	19	82.6	181	1	LGUL_EBRAJU	O44885
727	19	82.6	155	1	R73_LACLA	Q98q74	19	82.6	185	1	NRFB_ECOLI	P37207
728	19	82.6	155	1	R73_LACLA	Q98q74	19	82.6	185	1	NRFB_ECOLI	P37207
729	19	82.6	155	1	R73_MYCLE	P47334	19	82.6	188	1	NRFB_ECOLI	P37207
730	19	82.6	155	1	R73_MYCLE	P47334	19	82.6	188	1	NRFB_ECOLI	P37207
731	19	82.6	155	1	R73_MYCPN	Q8vmd1	19	82.6	189	1	APCD_RABIT	P37153
732	19	82.6	155	1	R73_MYCPN	Q8vmd1	19	82.6	189	1	APCD_RABIT	P37153
733	19	82.6	155	1	R73_MYCPU	P41194	19	82.6	190	1	YV22_HUMAN	O00597
734	19	82.6	155	1	R73_UREPA	Q9ppw6	19	82.6	190	1	YV22_HUMAN	O00597
735	19	82.6	156	1	ATPF_VIBCH	Q9knh1	19	82.6	192	1	YV22_HUMAN	O00597
736	19	82.6	156	1	ISPF_CLOPE	Q8xi08	19	82.6	192	1	YV22_HUMAN	O00597
737	19	82.6	156	1	R73_CYACA	Q9f1v7	19	82.6	192	1	YV22_HUMAN	O00597
738	19	82.6	156	1	R73_AGRTS	Q8ue14	19	82.6	192	1	YV22_HUMAN	O00597
739	19	82.6	156	1	R73_BACHD	Q92918	19	82.6	192	1	YV22_HUMAN	O00597
740	19	82.6	156	1	R73_CLOAB	Q97eh3	19	82.6	192	1	YV22_HUMAN	O00597
741	19	82.6	156	1	R73_CLOPE	Q8xhs0	19	82.6	192	1	YV22_HUMAN	O00597
742	19	82.6	156	1	R73_LISMO	Q927i4	19	82.6	192	1	YV22_HUMAN	O00597
743	19	82.6	156	1	R73_MICLU	P09898	19	82.6	192	1	YV22_HUMAN	O00597
744	19	82.6	156	1	R73_MYCBO	Q53539	19	82.6	192	1	YV22_HUMAN	O00597
745	19	82.6	156	1	R73_MYCPU	Q98gd7	19	82.6	192	1	YV22_HUMAN	O00597
746	19	82.6	156	1	R73_RHILU	Q98gd7	19	82.6	192	1	YV22_HUMAN	O00597
747	19	82.6	156	1	R73_RHIME	Q92gh3	19	82.6	192	1	YV22_HUMAN	O00597
748	19	82.6	156	1	R73_RHOCA	P50661	19	82.6	192	1	YV22_HUMAN	O00597
749	19	82.6	156	1	R73_STAAM	Q99w62	19	82.6	192	1	YV22_HUMAN	O00597
750	19	82.6	156	1	R73_STRCP	Q910k4	19	82.6	192	1	YV22_HUMAN	O00597
751	19	82.6	156	1	R73_STRP3	P59062	19	82.6	192	1	YV22_HUMAN	O00597
752	19	82.6	156	1	R73_STRPY	Q98ah2	19	82.6	192	1	YV22_HUMAN	O00597
753	19	82.6	156	1	R73_STRRP	P95847	19	82.6	192	1	YV22_HUMAN	O00597
754	19	82.6	156	1	R73_THICU	O50564	19	82.6	192	1	YV22_HUMAN	O00597
755	19	82.6	157	1	ISPF_LISIN	Q92f39	19	82.6	192	1	YV22_HUMAN	O00597
756	19	82.6	157	1	ISPF_LISMO	Q8yab4	19	82.6	192	1	YV22_HUMAN	O00597
757	19	82.6	157	1	R73_CAUCR	P93657	19	82.6	192	1	YV22_HUMAN	O00597
758	19	82.6	157	1	T2P2_PROVU	Q9ac14	19	82.6	192	1	YV22_HUMAN	O00597
759	19	82.6	157	1	Y054_CAUCR	O8g4q2	19	82.6	192	1	YV22_HUMAN	O00597
760	19	82.6	158	1	DTD_BIFLO	O87lq3	19	82.6	192	1	YV22_HUMAN	O00597
761	19	82.6	158	1	ISPF_VIBPA	O87lq3	19	82.6	192	1	YV22_HUMAN	O00597
762	19	82.6	158	1	ISPF_VIBVU	Q84c59	19	82.6	192	1	YV22_HUMAN	O00597
763	19	82.6	159	1	NUSB_PSEAE	Q9hwx6	19	82.6	192	1	YV22_HUMAN	O00597

837	19	82.6	227	1	6PGL_HELPY	O25730 helicobacte	910	19	82.6	288	1	PHZ2_MOUSE	Q9dc36 mus musculu
838	19	82.6	227	1	MAA2_DROME	Q9vhd3 drosophila	911	19	82.6	288	1	ZIPA_PSEMI	O87YV5 pseudomonas
839	19	82.6	227	1	MAD_MOUSE	P50538 mus musculu	912	19	82.6	288	1	YGAH_ECOLI	P25887 escherichia
840	19	82.6	227	1	NAPC_RHOSH	Q53178 rhodobacter	913	19	82.6	288	1	PNMT_MOUSE	P40935 mus musculu
841	19	82.6	228	1	RLI_THETH	P27150 thermus the	914	19	82.6	288	1	END4_STAEP	Q8c25 staphylococ
842	19	82.6	230	1	FLAH_METVO	O06641 methanococ	915	19	82.6	288	1	ZIPA_PSEPK	Q88f24 pseudomonas
843	19	82.6	232	1	PYRE_SORMA	P18904 sordaria ma	916	19	82.6	288	1	BYRF_USTMA	P11188 ustilago ma
844	19	82.6	233	1	HIS9_THEMEA	Q9wzr1 thermotoga	917	19	82.6	288	1	PHPC_PSEPA	P11122 pseudomonas
845	19	82.6	233	1	OP67_NEIGO	Q05034 neisseria g	918	19	82.6	288	1	HEM6_ECO57	O8xb14 escherichia
846	19	82.6	234	1	YVEK_BACSU	P71050 bacillus su	919	19	82.6	288	1	HEM6_ECOL6	O8ffa3 escherichia
847	19	82.6	236	1	IPTI_AGRVI	Q04590 agrobacteri	920	19	82.6	288	1	HEM6_ECOLI	P36553 escherichia
848	19	82.6	236	1	YJ26_YEAST	P47115 saccharomyc	921	19	82.6	288	1	HYPB_RHILV	P28155 rhizobium l
849	19	82.6	237	1	NAPC_PARPAN	Q56352 paracoccus	922	19	82.6	288	1	SPSY_YEAST	Q12455 saccharomyc
850	19	82.6	237	1	Y913_BACHD	Q9ked9 bacillus ha	923	19	82.6	288	1	NAHC_PSEAE	Q57145 pseudomonas
851	19	82.6	237	1	YG6C_ECOLI	P11664 escherichia	924	19	82.6	288	1	HYPB_AZOVI	P31880 azotobacter
852	19	82.6	238	1	OP66_NEIGO	Q05033 neisseria g	925	19	82.6	288	1	HYPB_AZOCH	Q43949 azotobacter
853	19	82.6	238	1	BBP_CHICK	P02752 gallus gall	926	19	82.6	288	1	YG5T_YEAST	P53332 saccharomyc
854	19	82.6	239	1	DCUR_ECOL6	P59338 escherichia	927	19	82.6	288	1	ARGC_DEIRA	Q9ry72 deinococcus
855	19	82.6	239	1	DCUR_ECOLI	P39271 escherichia	928	19	82.6	288	1	GLS2_MYCLE	Q49807 mycobacteri
856	19	82.6	239	1	DCUR_SHIFL	P59339 shigella fl	929	19	82.6	288	1	OPPF_STEMU	Q82p12 salmonella
857	19	82.6	244	1	CYSH_PHOLL	Q7mb85 photorhabdu	930	19	82.6	288	1	PLD_ARCHA	P72479 streptococc
858	19	82.6	244	1	RS2_BACHD	Q9ka63 bacillus ha	931	19	82.6	288	1	SC65_YARLI	Q59121 arcanobacte
859	19	82.6	245	1	YGZA_YEAST	P53060 saccharomyc	932	19	82.6	288	1	VE2_HPV56	P41922 yarrowia li
860	19	82.6	247	1	FABG_MYCTU	Q48930 mycobacteri	933	19	82.6	288	1	YF85_METJA	P36798 human papil
861	19	82.6	247	1	GRAN_GVAS	P31035 agrotis seg	934	19	82.6	288	1	OYJ3_HUMAN	Q58980 methanococ
862	19	82.6	248	1	WCAE_ECOLI	P71239 escherichia	935	19	82.6	288	1	TXTP_BOVIN	Q8nh60 homo sapien
863	19	82.6	249	1	RTLD_MOUSE	Q9ji58 mus musculu	936	19	82.6	288	1	TXTP_HUMAN	P79110 bos taurus
864	19	82.6	251	1	RTLE_MOUSE	Q9c2q6 mus musculu	937	19	82.6	288	1	TXTP_HUMAN	P53007 homo sapien
865	19	82.6	252	1	TPIS_NITEU	Q82tut nitrosomona	938	19	82.6	288	1	TXTP_RAT	P2089 rattus norv
866	19	82.6	253	1	CYSZ_SHIFL	Q83gm8 shigella fl	939	19	82.6	288	1	1A1D_THEMEA	Q9wy68 thermotoga
867	19	82.6	253	1	GLBL_TYLHE	P18207 tylosynchyl	940	19	82.6	288	1	RIR2_RSIV	Q9qt62 red sea bre
868	19	82.6	253	1	RT1A_MOUSE	O08602 mus musculu	941	19	82.6	288	1	MER2_YEAST	P21651 saccharomyc
869	19	82.6	253	1	RT1B_MOUSE	O08603 mus musculu	942	19	82.6	288	1	REP_LACHI	P35857 lactobacill
870	19	82.6	253	1	RT1C_MOUSE	O08604 mus musculu	943	19	82.6	288	1	YDQC_SCHPO	Q14204 schizosacch
871	19	82.6	253	1	SURE_ECOLI	P36664 escherichia	944	19	82.6	288	1	T2R3_HUMAN	Q9nyw6 homo sapien
872	19	82.6	253	1	SURE_SHIFL	Q83jy2 shigella fl	945	19	82.6	288	1	Y3SK_HALSG	P17565 halobacteri
873	19	82.6	254	1	ETFB_SCHPO	Q9uth2 schizosacch	946	19	82.6	288	1	FECR_ECOLI	P23485 escherichia
874	19	82.6	254	1	RS2_OETH	O8egv3 oceanobacil	947	19	82.6	288	1	YVCK_BACSU	O06974 bacillus su
875	19	82.6	255	1	FABG_MYCAV	O07399 mycobacteri	948	19	82.6	288	1	COAA_BACSU	P54556 bacillus su
876	19	82.6	255	1	FABG_MYCSM	P71534 mycobacteri	949	19	82.6	288	1	CYF_WARPO	P06246 marchantia
877	19	82.6	255	1	FOLI_MOUSE	P35846 mus musculu	950	19	82.6	288	1	MRAW_HAFIN	P45057 haemophilus
878	19	82.6	255	1	GAG_IPMAE	P31790 mouse intra	951	19	82.6	288	1	Y486_METJA	Q57910 methanococ
879	19	82.6	256	1	YAFV_ECOLI	Q47679 escherichia	952	19	82.6	288	1	CDC2_EWENI	O06246 emeritella
880	19	82.6	257	1	FOLI_HUMAN	P15328 homo sapien	953	19	82.6	288	1	CITG_HARDU	Q30827 haemophilus
881	19	82.6	257	1	NOCP_AGRTS	P35116 agrobacteri	954	19	82.6	288	1	LUKF_STAAR	P31715 staphylococ
882	19	82.6	260	1	HIS9_DEIRA	Q9rx45 deinococcus	955	19	82.6	288	1	ANXA_HUMAN	Q9uj72 homo sapien
883	19	82.6	261	1	TATD_ECOLI	P27859 escherichia	956	19	82.6	288	1	ANXA_MOUSE	Q9qz10 mus musculu
884	19	82.6	261	1	KLK1_RAT	P00758 rattus norv	957	19	82.6	288	1	CDC2_AJECA	P54119 ajellomyces
885	19	82.6	262	1	RS2_ENTFA	Q831u9 enterococcu	958	19	82.6	288	1	BLAI_STRCI	Q03680 streptomyc
886	19	82.6	262	1	YU05_MYCGE	P47255 mycoplasma	959	19	82.6	288	1	HLGB_STAAN	Q07226 staphylococ
887	19	82.6	262	1	YU48_ENTFA	P59745 enterococcu	960	19	82.6	288	1	YOLC_BACSU	P42414 bacillus su
888	19	82.6	263	1	YH25_DEIRA	O83030 deinococcus	961	19	82.6	288	1	K6PF_SPLIC	P20275 spiroplasma
889	19	82.6	265	1	DCMR_METSP	P45876 methylolact	962	19	82.6	288	1	G3P_KLUJA	P17819 kluyveromyc
890	19	82.6	268	1	HIS9_BACSU	Q34411 bacillus su	963	19	82.6	288	1	SQV7_CABEL	P18779 caenorhabd
891	19	82.6	272	1	RS2_CORGL	Q8np01 corynebacte	964	19	82.6	288	1	G3P2_YEAST	P00358 saccharomyc
892	19	82.6	272	1	VAL1_MSVK	P03568 maize strea	965	19	82.6	288	1	G3P_CANAL	Q92211 candida alb
893	19	82.6	272	1	VAL1_MSVN	P14980 maize strea	966	19	82.6	288	1	LDHA_MONDO	Q9xt87 monodelphis
894	19	82.6	272	1	VAL1_MSVS	P14990 maize strea	967	19	82.6	288	1	LDHA_SCEUN	Q9w715 sceloporu
895	19	82.6	273	1	HIS9_BACHD	Q9k801 bacillus ha	968	19	82.6	288	1	DUSA_PSEAE	Q91048 pseudomonas
896	19	82.6	273	1	PRXC_PSEFL	Q31158 pseudomonas	969	19	82.6	288	1	LDHA_RAT	P04642 rattus norv
897	19	82.6	274	1	NADE_LISIN	Q92cu3 listeria in	970	19	82.6	288	1	YC56_PASMU	Q9clh5 pasteurella
898	19	82.6	274	1	NADE_LISMO	Q8v825 listeria mo	971	19	82.6	288	1	YIAK_HAFIN	P44995 haemophilus
899	19	82.6	275	1	HPCB_ECOLI	Q05353 escherichia	972	19	82.6	288	1	LDHB_BRARE	Q9pvk4 brachydanio
900	19	82.6	275	1	NADE_STAEP	Q8cnpl staphylococ	973	19	82.6	288	1	ILVC_METJA	Q58938 methanococ
901	19	82.6	275	1	YCT7_YEAST	P25627 saccharomyc	974	19	82.6	288	1	LDHB_SQUAC	Q9y105 aqualus aca
902	19	82.6	276	1	RS2_COREF	Q8fp70 corynebacte	975	19	82.6	288	1	LPXK_VIBVO	Q8davi vibrio vuln
903	19	82.6	281	1	PANB_MYCTU	Q10505 mycobacteri	976	19	82.6	288	1	STXH_HUMAN	Q9p2w9 homo sapien
904	19	82.6	281	1	PANC_CLOAB	Q97f38 clostridium	977	19	82.6	288	1	LDHD_LACHE	P30901 lactobacill
905	19	82.6	285	1	OPF3_NPVOP	P90212 oryza pseeu	978	19	82.6	288	1	YERT_BACSU	Q34640 bacillus su
906	19	82.6	285	1	PNMT_RAT	P10937 rattus norv	979	19	82.6	288	1	G3PI_AGABI	P22675 agaricus bi
907	19	82.6	287	1	RP32_BUCBP	Q89b27 buchnera ap	980	19	82.6	288	1	RL3_HALMA	P32079 haloarcula
908	19	82.6	287	1	SYGA_CAMJE	Q9ppk3 campylobact	981	19	82.6	288	1	ILVC_BRUME	Q8y121 brucella me
909	19	82.6	288	1	PHZ1_MOUSE	Q9cxn7 mus musculu	982	19	82.6	288	1	ILVC_BRUSE	Q8fzui brucella su

983 19 82.6 340 1 GLSA\_YERPE  
 984 19 82.6 341 1 PAFR\_MOUSE  
 985 19 82.6 341 1 PAFR\_RAT  
 986 19 82.6 342 1 ILVC\_BACSU  
 987 19 82.6 342 1 PAFR\_CAVPO  
 988 19 82.6 342 1 PAFR\_HUMAN  
 989 19 82.6 344 1 HMD\_METTF  
 990 19 82.6 344 1 HMD\_METTF  
 991 19 82.6 344 1 HMD\_METTF  
 992 19 82.6 344 1 HMD\_METTF  
 993 19 82.6 344 1 RPF2\_YEAST  
 994 19 82.6 345 1 OGG1\_HUMAN  
 995 19 82.6 345 1 OGG1\_MOUSE  
 996 19 82.6 345 1 OGG1\_RAT  
 997 19 82.6 345 1 OUEA\_HELPJ  
 998 19 82.6 345 1 OUEA\_HELPY  
 999 19 82.6 346 1 TPA3\_LEPPO  
 1000 19 82.6 347 1 HDL1\_HUMAN

## ALIGNMENTS

RESULT 1  
 ID PTIA\_STRMU STANDARD; PRT; 104 AA.  
 AC P26426;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE PTS system, lactose-specific IIA component (EIIA-LAC) (Lactose-  
 permease IIA component) (Phosphotransferase enzyme II, A component)  
 DE (EC 2.7.1.69) (EIIA-LAC).  
 GN LACF OR SMU.1492.

OS Streptococcus mutans.  
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 OC Streptococcus.

NCBI\_TaxID=11309;  
 [1]

RP SEQUENCE FROM N.A.  
 EX MEDLINE=93015655; PubMed=1400164;

RA Rosey E.L., Stewart G.C.;  
 RT "Nucleotide and deduced amino acid sequences of the lacR, lacABCD,  
 RT and lacFE genes encoding the repressor, tagatose 6-phosphate gene  
 RT cluster, and sugar-specific phosphotransferase system components of  
 RT the lactose operon of Streptococcus mutans.";  
 RL J. Bacteriol. 174:6159-6170(1992).  
 [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN=UA159 / ATCC 700610 / Serotype C;  
 RX MEDLINE=22295063; PubMed=12397186;  
 RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,  
 RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y.,  
 RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;  
 RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental  
 RT pathogen.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).

CC -!- FUNCTION: This is a component of the phosphoenolpyruvate-dependent  
 CC sugar phosphotransferase system (PTS), a major carbohydrate active  
 CC -transport system. The IID domains contain the sugar binding site  
 CC and the transmembrane channel; the IIA domain contains the primary  
 CC phosphorylation site (the donor is phospho-HPr); IIA transfers its  
 CC phosphoryl group to the IIB domain which finally transfers it to  
 CC the sugar.  
 CC -!- CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein  
 CC histidine + sugar phosphate.  
 CC -!- COFACTOR: Binds 1 magnesium or manganese ion per trimer (By  
 CC similarity).  
 CC -!- SUBUNIT: Homotrimer.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: Contains 1 PTS EIIA domain.

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EMBL; M80797; AAA26908.1; -;  
 EMBL; AE014981; AAN59146.1; -;  
 DR PIR; G43258; G43258.  
 DR HSSP; P23532; 1E2A.

DR InterPro; IPR003188; Ptrans\_IIA.  
 DR Pfam; PF02255; PTS\_IIA; 1.  
 DR ProDom; PD007286; PTS\_IIA; 1.

DR TIGRFAMs; TIGR00823; EIIA-LAC; 1.

KW Phosphotransferase system; Sugar transport; Transferase;

KW Phosphorylation; Metal-binding; Magnesium; Manganese;

KW Complete proteome.

FT METAL 81  
 FT MOD RES 78 78  
 SQ SEQUENCE 104 AA; 11399 MW; 281CB2F3CB109F5D CRC64;

Query Match 100.0%; Score 23; DB 1; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4

DB 52 DAHK 55

## RESULT 2

Y210 COREF

ID Y210 COREF STANDARD; PRT; 107 AA.

AC Q8FUI1,

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Hypothetical UPF0133 protein CE0210.

GN CE0210

OS Corynebacterium efficiens.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.

OC NCBI\_TaxID=152794;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

RX MEDLINE=22723752; PubMed=12840036;

RA Nishio Y., Nakamura Y., Kawarayashi Y., Usuda Y., Kimura E.,

RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,

RA Gojibori T.;

RT "Comparative complete genome sequence analysis of the amino acid  
 RT replacements responsible for the thermostability of Corynebacterium  
 RT efficiens.";

RL Genome Res. 13:1572-1579(2003).

CC -!- SUBUNIT: Homodimer (By similarity).

CC -!- SIMILARITY: Belongs to the UPF0133 family.

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EMBL; AP005214; BAC17020.1; ALT\_INIT.

DR HAMAP; MF\_00274; -; 1.

DR InterPro; IPR004401; Cons\_hypoth103.

DR Pfam; PF02575; DUF149; 1.

DR TIGRFAMs; TIGR00103; TIGR00103; 1.

KW Hypothetical protein; Complete proteome

SQ SEQUENCE 107 AA; 11160 MW; 288F22C385CAC6B8 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 DB 79 DAHK 82

## RESULT 3

RBFA\_RANES STANDARD; PRT; 116 AA.  
 ID RBFA\_UREFA  
 AC QPQH0;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE Ribosome-binding factor A.  
 DR RBFA OR U0321.

OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.  
 OX NCBI\_TaxID=134821;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Serovar 3;  
 RX MEDLINE=20500219; PubMed=11048724;  
 RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,  
 RA Cassell G.H.;

RT "The complete sequence of the mucosal pathogen Ureaplasma

urealyticum.";

RL Nature 407:757-762 (2000).

CC -!- FUNCTION: Associates with free 30S ribosomal subunits (but not  
 with 30S subunits that are part of 70S ribosomes or polysomes).  
 Essential for efficient processing of 16S rRNA. May interact with  
 the 5' terminal helix region of 16S rRNA (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

CC -!- SIMILARITY: Belongs to the rbfA family.

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DR EMBL; AE002129; AAF30730.1; -

DR HAMAP; MF 00003; -; 1.

DR InterPro; IPR000238; Rib\_bind\_factA.

DR Pfam; PF02033; RBFA; 1.

DR ProDom; PD007327; Rib\_bind\_factA; 1.

DR TIGRFAMs; TIGR00082; rbfA; 1.

DR PROSITE; PS01319; RBFA; FALSE NEG.

KW rRNA processing; Complete proteome.

SQ SEQUENCE 116 AA; 13247 MW; A79DCC71F0547514 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 DB 53 DAHK 56

## RESULT 4

HBB\_RANES STANDARD; PRT; 140 AA.  
 ID HBB\_RANES  
 AC P02134;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.

GN HBB.  
 OS Rana esculenta (Edible frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranae;  
 OX NCBI\_TaxID=8401;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=72111329; PubMed=4536743;  
 RA Chauvet J.-P., Acher R.;  
 RT "Phylogeny of hemoglobins. Beta chain of frog (*Rana esculenta*)  
 hemoglobin.";  
 RL Biochemistry 11:916-927 (1972).  
 CC -!- FUNCTION: Involved in oxygen transport from the lung to the  
 various peripheral tissues.  
 CC -!- SUBUNIT: Heterotetramer of two alpha chains and two beta chains.  
 CC -!- TISSUE SPECIFICITY: Red blood cells.  
 CC -!- SIMILARITY: Belongs to the globin family.

DR PIR; A02454; HBBGRE.  
 DR HSSP; P02023; 1BAB.  
 DR InterPro; IPR002337; Beta haem.  
 DR InterPro; IPR000971; Globin.  
 DR Pfam; PF00042; globin; 1.  
 DR PRINTS; PR00814; BETAHAEM.  
 DR PROSITE; PS01033; GLOBIN; 1.  
 KW Heme; Oxygen transport; Transport; Erythrocyte.  
 FT METAL 57 57 IRON (HEME DISTAL LIGAND).  
 FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).  
 SQ SEQUENCE 140 AA; 15423 MW; 151F75CF7076AAB0 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 140;  
 Best Local Similarity 100.0%; Pred. No. 57;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 DB 13 DAHK 16

## RESULT 5

FUR\_VIBPA

ID FUR\_VIBPA STANDARD; PRT; 149 AA.

AC 024755;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ferric uptake regulation protein (ferric uptake regulator).

GN FUR OR VP0833.

OS Vibrio parahaemolyticus.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrio.

OX NCBI\_TaxID=670;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RIMD WPI;

RX MEDLINE=98003754; PubMed=9343826;

RA Yamamoto S., Funahashi T., Ikai F., Shinoda S.;

RT "Cloning and sequencing of the Vibrio parahaemolyticus fur gene.";

RL Microbiol. Immunol. 41:737-740 (1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=RIMD 2210633 / Serotype O3:K6;

RX MEDLINE=22508454; PubMed=12620739;

RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.;

RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.;

RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism

distinct from that of *V. cholerae*.";

RL Lancet 361:743-749 (2003).

CC -!- FUNCTION: FUR ACTS AS A REPRESSOR, EMPLOYING FE(2+) AS A COFACTOR

TO BIND THE OPERATOR OF THE IRON TRANSPORT OPERON.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the Fur family.

CC -----

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DR EMBL; AB003752; BAA22785.1; -;  
 DR EMBL; AP005075; BAC59096.1; -;  
 DR InterPro: IPR002481; FUR.  
 DR Pfam; PF01475; FUR; 1.  
 DR ProDom; P0002003; FUR; 1.  
 KW Transcription regulation; Repressor; DNA-binding; Iron; Zinc;  
 KW Complete proteome.  
 FT DOMAIN 86 90 HIS-RICH.  
 FT METAL 93 93 ZINC (BY SIMILARITY).  
 FT METAL 96 96 ZINC (BY SIMILARITY).  
 SQ SEQUENCE 149 AA; 16771 MW; 72E66238380D36BD CRC64;

Query Match 100.0%; Score 23; DB 1; Length 149;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 Db 143 DAHK 146

## RESULT 6

FUR\_VIBVU STANDARD; PRT; 149 AA.  
 ID FUR\_VIBVU  
 AC P33117;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ferric uptake regulation protein (Ferric uptake regulator).  
 OS FUR OR V10175.  
 GN Vibrio vulnificus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=672;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93139039; PubMed=7678593;  
 RA Litwin C.M., Calderwood S.B.;  
 RA "Cloning and genetic analysis of the Vibrio vulnificus fur gene and  
 RT construction of a fur mutant by in vivo marker exchange."  
 RL J. Bacteriol. 175:706-715(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=CMCP6;  
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
 RA Choy H.E.;  
 RT "Complete genome sequence of Vibrio vulnificus CMCP6."  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: FUR ACTS AS A REPRESSOR, EMPLOYING FE(2+) AS A COFACTOR  
 CC TO BIND THE OPERATOR OF THE IRON TRANSPORT OPERON.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the Fur family.

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DR EMBL; L06428; AAA27521.1; -;  
 DR EMBL; AE016797; AAC08713.1; -;  
 DR PIR; A47054; A47054.  
 DR InterPro: IPR002481; FUR.

DR Pfam; PF01475; FUR; 1.  
 DR ProDom; P0002003; FUR; 1.  
 KW Transcription regulation; Repressor; DNA-binding; Iron; Zinc;  
 KW Complete proteome.  
 FT DOMAIN 86 90 HIS-RICH.  
 FT METAL 93 93 ZINC (BY SIMILARITY).  
 FT METAL 96 96 ZINC (BY SIMILARITY).  
 FT CONFLICT 149 149 N -> S (IN REF. 1).  
 SQ SEQUENCE 149 AA; 16743 MW; 3C54EBB82C0F21C8 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 149;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 Db 143 DAHK 146

## RESULT 7

HUTP\_BACSU STANDARD; PRT; 151 AA.  
 ID HUTP\_BACSU  
 AC P10943;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hut operon positive regulatory protein.  
 GN HUTP OR BSU3340.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8257040; PubMed=2454913;  
 RA Oda M., Sugishita A., Furukawa K.;  
 RA "Cloning and nucleotide sequences of histidase and regulatory genes  
 RT in the Bacillus subtilis hut operon and positive regulation of the  
 RL operon."  
 RL J. Bacteriol. 170:3199-3205(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=168 / BGSC1A1;  
 RC MEDLINE=95219088; PubMed=7704263;  
 RA Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;  
 RA "Cloning and sequencing of a 29 kb region of the Bacillus subtilis  
 RT genome containing the hut and wpa loci."  
 RL Microbiology 141:337-343(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN=168;  
 RC MEDLINE=98044033; PubMed=9384377;  
 RA Kunst F., Ogawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borcherdt S.,  
 RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,  
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., N.,  
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,  
 RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Hollappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Mostl D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
 RA Presecan E., Pujić P., Purnelle B., Rapoport G., Rev M., Reynolds S.,  
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,  
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,



RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,  
RA Winters P., Wipat A., Yamamoto H., Yanane K., Yasumoto K., Yata K.,  
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,  
RT "The complete genome sequence of the Gram-positive bacterium Bacillus  
subtilis";  
RL Nature 390:249-256 (1997).  
CC -!- FUNCTION: POSITIVE REGULATOR OF THE HISTIDINE UTILIZATION (HUT)  
CC OPERON.  
CC  
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CC  
CC EMBL; M20659; AAA22537.1; -;  
CC EMBL; D31856; BAA06645.1; -;  
CC EMBL; Z99124; CAB15970.1; -;  
CC PIR; S18809; RGSHP.  
CC Subtilist; BG10666; hutP.  
CC Histidine metabolism; Transcription regulation; Activator;  
CC DNA-binding; Complete proteome.  
CC SEQUENCE 151 AA; 16577 MW; E27ABDA7A533C35D CRC64;  
CC  
CC Query Match 100.0%; Score 23; DB 1; Length 151;  
CC Best Local Similarity 100.0%; Pred. No. 62;  
CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CC  
CC QY 1 DAHK 4  
CC Db 49 DAHK 52  
CC  
CC RESULT 8  
CC ATPF\_VIBVU STANDARD; PRT; 156 AA.  
CC AC Q8DDH2;  
CC DT 15-MAR-2004 (Rel. 43, Created)  
CC DT 15-MAR-2004 (Rel. 43, Last sequence update)  
CC DT 15-MAR-2004 (Rel. 43, Last annotation update)  
CC DE ATP synthase B chain (EC 3.6.3.14).  
CC GN ATPF OR VV11017.  
CC OS Vibrio vulnificus.  
CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
CC OC Vibrionaceae; Vibrio.  
CC OX NCBI\_TaxID=672;  
CC RN [1]  
CC SEQUENCE FROM N.A.  
CC RC STRAIN=CMCP6;  
CC RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
CC Choy H.E.;  
CC RT "Complete genome sequence of Vibrio vulnificus CMCP6.";  
CC RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +  
CC H(+) (Out).  
CC -!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic  
CC core - and CF(0) - the membrane proton channel. CF(1) has five  
CC subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)  
CC has three main subunits: a, b and c (By similarity).  
CC -!- SIMILARITY: Belongs to the ATPase B chain family.  
CC  
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CC

CC EMBL; AE016800; AAO09505.1; ALT INIT.  
CC InterPro; IPR002146; ATPynt B/E' sub.  
CC InterPro; IPR005864; ATP\_synthF0\_B.  
CC Pfam; PF00430; ATP-synt\_B; 1.  
CC TIGRFAMs; TIGR01144; ATP synt\_b; 1.  
CC KW Hydrogen ion transport; Transmembrane; CF(0); Complete proteome.  
CC FT TRANSMEM 2 22 POTENTIAL.  
CC SQ SEQUENCE 156 AA; 17562 MW; 01FE27B4F037ALB0 CRC64;  
CC  
CC Query Match 100.0%; Score 23; DB 1; Length 156;  
CC Best Local Similarity 100.0%; Pred. No. 64;  
CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CC  
CC QY 1 DAHK 4  
CC Db 143 DAHK 146  
CC  
CC RESULT 9  
CC LCRH\_YERPE STANDARD; PRT; 168 AA.  
CC ID LCRH\_YERPE  
CC AC P21207;  
CC DT 01-MAY-1991 (Rel. 18, Created)  
CC DT 01-MAY-1991 (Rel. 18, Last sequence update)  
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)  
CC DE Low calcium response locus protein H.  
CC GN LCRH OR YPCD1.30C OR Y5048 OR Y0051.  
CC OS Yersinia pestis.  
CC OG Plasmid pCD1.  
CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
CC OC Enterobacteriaceae; Yersinia.  
CC OX NCBI\_TaxID=632;  
CC RN [1]  
CC SEQUENCE FROM N.A.  
CC RC STRAIN=KIM5 / Biovar Mediaevalis;  
CC RX MEDLINE=9000806; PubMed=2477361;  
CC RA Price S.B., Leung K.Y., Barve S.S., Straley S.C.;  
CC RT "Molecular analysis of lcrGVH, the V antigen operon of Yersinia  
CC pestis";  
CC RL J. Bacteriol. 171:5646-5653 (1989).  
CC RN [2]  
CC SEQUENCE FROM N.A.  
CC RC STRAIN=KIM5 / Biovar Mediaevalis;  
CC RX MEDLINE=98427122; PubMed=9746557;  
CC RA Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,  
CC Blattner F.R.;  
CC RT "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of  
CC Yersinia pestis KIM5.";  
CC RL Infect. Immun. 66:4611-4623 (1998).  
CC RN [3]  
CC SEQUENCE FROM N.A.  
CC RC STRAIN=KIM5 / Biovar Mediaevalis;  
CC RX MEDLINE=98422474; PubMed=9748454;  
CC RA Hu P., Elliott J., McCready P., Skowronski E., Ganes J.,  
CC Kobayashi A., Brubaker R.R., Garcia E.;  
CC RT "Structural organization of virulence-associated plasmids of Yersinia  
CC pestis";  
CC RL J. Bacteriol. 180:5192-5202 (1998).  
CC RN [4]  
CC SEQUENCE FROM N.A.  
CC RC STRAIN=CO-92 / Biovar Orientalis;  
CC RX MEDLINE=21470413; PubMed=11586360;  
CC RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,  
CC RA Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,  
CC RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Farraga A.M.,  
CC RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,  
CC RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,  
CC RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,  
CC RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;  
CC RT "Genome sequence of Yersinia pestis, the causative agent of plague.";  
CC RL Nature 413:523-527 (2001).  
CC -!- FUNCTION: MEDIATES THE NEGATIVE REGULATION OF THE LCRGVH OPERON BY  
CC

ATP OR CA(2+). ACTS AS A MODULATOR OF THE YOP OPERON EXPRESSION.  
 -!- SIMILARITY: TO SHIGELLA INVASION PLASMID IPPI PROTEIN.

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 EMBL; M26405; AAC27642.1; -  
 EMBL; AF074612; AAC69800.1; -  
 EMBL; AF053946; AAC62575.1; -  
 EMBL; AL117189; CAB54907.1; -  
 PIR; C33601; C33601.  
 InterPro; IPR008940; Prenyl\_trans.  
 InterPro; IPR005415; SycD\_chap.  
 InterPro; IPR001440; TPR.  
 PRINTS; PR01595; SYCDCHAPRONE.  
 Plasmid; Complete proteome.  
 SQ SEQUENCE 168 AA; 19014 MW; 46206AF240EB0064 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 168;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 DB 54 DAHK 57

RESULT 10  
 LCRH YERPS STANDARD; PRT; 168 AA.  
 AC P23995;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Low calcium response locus protein H.  
 GN LCRH.  
 OS Yersinia pseudotuberculosis.  
 OG Plasmid pIB1.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Yersinia.  
 OX NCBI\_TaxID=633;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=YPIII;  
 RX MEDLINE=91154114; PubMed=1705541;  
 RA Bergman T., Haakanson S., Forsberg A., Norlander L., Macellaro A.,  
 RA Baekman A., Boelin I., Wolf-Watz H.;  
 RT "Analysis of the V antigen lcrGVH-yopBD operon of Yersinia  
 pseudotuberculosis: evidence for a regulatory role of LcrH and  
 LcrV.";  
 RT LcrV.";  
 RL J. Bacteriol. 173:1607-1616(1991).  
 CC -!- FUNCTION: MEDIATES THE NEGATIVE REGULATION OF THE LCRGVH OPERON BY  
 ATP OR CA(2+). ACTS AS A MODULATOR OF THE YOP OPERON EXPRESSION.  
 CC -!- SIMILARITY: TO SHIGELLA INVASION PLASMID IPPI PROTEIN.

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 EMBL; M57893; AAA27646.1; -  
 PIR; C37314; C37314.  
 InterPro; IPR008940; Prenyl\_trans.  
 InterPro; IPR005415; SycD\_chap.  
 InterPro; IPR001440; TPR.

DR PRINTS; PR01595; SYCDCHAPRONE.  
 KW Plasmid.  
 SQ SEQUENCE 168 AA; 19010 MW; 2CE06AF240EB0424 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 168;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 DB 54 DAHK 57

RESULT 11  
 PHAF CYACA STANDARD; PRT; 170 AA.  
 ID PHAF CYACA  
 AC O19896;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Allophycocyanin beta 18 chain.  
 GN APCF.  
 OS Cyanidium caldarium.  
 OG Chloroplast.  
 OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;  
 OC Cyanidium.  
 OX NCBI\_TaxID=2771;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RK-1;  
 RX MEDLINE=20496959; PubMed=11040290;  
 RA Gloeckner G., Rosenthal A., Valentin K.-U.;  
 RT "The structure and gene repertoire of an ancient red algal plastid  
 genome.";  
 RL J. Mol. Evol. 51:382-390(2000).  
 CC -!- FUNCTION: Light-harvesting photosynthetic bile pigment-protein  
 from the phycobiliprotein complex. Allophycocyanin has a maximum  
 absorption at approximately 650 nanometers.  
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.  
 CC -!- PTM: Contains one covalently linked bilin chromophore.

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 EMBL; AF022186; AAB82693.1; -  
 PIR; T11964; T11964.  
 HSP; P00318; I833.  
 InterPro; IPR006245; ApcB.  
 InterPro; IPR001659; Phycobilisome.  
 Pfam; PF00502; Phycobilisome; 1.  
 ProDom; PD000340; Phycobilisome; 1.  
 TIGRfams; TIGR01337; apcB; 1.  
 DR Phycobilisome; Electron transport; Photosynthesis; Bile pigment;  
 KW Chloroplast; Methylation.  
 FT MOD RES 74 84  
 FT BINDING 84 84 METHYLATION (BY SIMILARITY).  
 FT PHYCOCYANOBILIN CHROMOPHORE (BY  
 FT SIMILARITY).  
 SQ SEQUENCE 170 AA; 19231 MW; 24914859DC69B185 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 70;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 DB 149 DAHK 152

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RESULT 12
IPYR_BRAJA STANDARD; PRT; 178 AA.
AC Q89WY0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
DE hydrolase) (PPase).
OS PPA OR BLR0548.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484988; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiyumi T.,
RA Sasamoto S., Watanabe A., Iodesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsunoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -!- COFACTOR: Binds 4 magnesium ions per subunit. Other metal ions can
CC support activity, but at a lower rate. Two magnesium ions are
CC required for the activation of the enzyme and are present before
CC substrate binds, two additional magnesium ions form complexes with
CC substrate and product (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the PPase family.
CC
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF005936; BAC45813.1; -.
DR HAMAP; MF_00209; -.
DR InterPro; IPR008163; Inorg_pphsp.
DR InterPro; IPR008162; Pyrophosphatase.
DR Pfam; PF00719; Pyrophosphatase; 1.
DR ProDom; PD002014; Inorg_pphsp; 1.
DR PROSITE; PS00387; PPASE; FALSE_NEG.
KW Hydrolase; Metal-binding; Magnesium; Complete proteome.
FT METAL 66 66 MAGNESIUM 1 (BY SIMILARITY).
FT METAL 71 71 MAGNESIUM 1 AND 2 (BY SIMILARITY).
FT METAL 103 103 MAGNESIUM 1 (BY SIMILARITY).
SQ SEQUENCE 178 AA; 20052 MW; EF8FBDF15D51EB1 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4
Db 161 DAHK 164

RESULT 13
SODF_TETPY STANDARD; PRT; 196 AA.
AC P19666;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1).
OS Tetrahymena pyriformis.

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OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymena; Tetrahymena.
OX NCBI_TaxID=5908;
RN [1]
RP SEQUENCE.
RX MEDLINE=91009226; PubMed=2170391;
RA Barra D., Schinina M.E., Bossa F., Puget K., Durosay P., Guissani A.,
RA Michelson A.M.;
RT "A tetrameric iron superoxide dismutase from the eucaryote
RT Tetrahymena pyriformis.";
RL J. Biol. Chem. 285:17680-17687(1990).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC PIR; A39223; A39223.
DR HSP; P04179; 1AP6.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR Pfam; PF02777; sodfe; 1.
DR PRINTS; PR01703; MNSODISMTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD MN; 1.
KW Oxidoreductase; Metal-binding; Iron.
FT METAL 20 20 IRON (BY SIMILARITY).
FT METAL 68 68 IRON (BY SIMILARITY).
FT METAL 157 157 IRON (BY SIMILARITY).
FT METAL 161 161 IRON (BY SIMILARITY).
SQ SEQUENCE 196 AA; 22657 MW; FC1P2F67893D8DC7 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4
Db 47 DAHK 50

RESULT 14
UBAL_CANAL STANDARD; PRT; 205 AA.
AC P52495;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ubiquitin-activating enzyme E1 1 (Fragment).
GN UBAL
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WO-1;
RA Raymond M., Dignard D., Mainville N., Magee B.B., Thomas D.Y.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Activates ubiquitin by first adenylating with ATP its
CC carboxy-terminal glycine residue and thereafter linking this
CC residue to the side chain of a cysteine residue in E1, yielding an
CC ubiquitin-E1 thioester and free AMP (By similarity).
CC -!- PATHWAY: Ubiquitin conjugation; first step.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC -!- MISCELLANEOUS: There are two active sites within the E1 molecule,
CC allowing it to accommodate two ubiquitin moieties at a time, with a
CC new ubiquitin forming an adenylate intermediate as the previous
CC one is transferred to the thiol site (By similarity).
CC -!- SIMILARITY: Belongs to the ubiquitin-activating E1 family.
CC

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Job time : 45 s3cs

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CC -----

DR EMBL; U13193; AAC49911.1; -  
DR PIR; T18215; T18215.  
DR InterPro; IPR000127; Ubact\_repeat.  
DR InterPro; IPR000011; Ugtin\_activ\_enz.  
DR Pfam; PF02134; UBACT; 1.  
DR PROSITE; PS00536; UBIQUITIN\_ACTIVAT\_1; PARTIAL.  
DR PROSITE; PS00865; UBIQUITIN\_ACTIVAT\_2; PARTIAL.  
KW Ub1 conjugation pathway; Ligase.  
FT NON TER 1  
SQ SEQUENCE 205 AA; 23166 MW; CD3F5EA99D0D2697 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 205;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAKH 4  
|  
|  
|  
|  
DB 32 DAKH 35

## RESULT 15

VG66\_BFMLS  
ID VG66\_BFMLS STANDARD; PRT; 207 AA.  
AC Q05280;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE Gene 66 protein (GP66).  
GN 66.  
OS Mycobacteriophage L5.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
OC L5-like viruses.  
OX NCBI\_TaxID=31757;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93211282; PubMed=8459766;  
RA Hatfull G.F., Sarkis G.J.;  
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:  
RT a phage system for mycobacterial genetics.";  
RL Mol. Microbiol. 7:395-405(1993).  
CC -----

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CC -----

DR EMBL; Z18946; CAA79442.1; -  
DR PIR; S31011; S31011.  
DR InterPro; IPR004843; M-peptase.  
DR Pfam; PF00149; Metallophos; 1.  
SQ SEQUENCE 207 AA; 23581 MW; 668BF8C639C7B20C CRC64;

Query Match 100.0%; Score 23; DB 1; Length 207;  
Best Local Similarity 100.0%; Pred. No. 86;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAKH 4  
|  
|  
|  
|  
DB 92 DAKH 95

Search completed: September 9, 2004, 23:45:38

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 9, 2004, 23:45:44 ; Search time 128 Seconds  
(without alignments)  
10.022 Million cell updates/sec

Title: US-10-076-071-1

Perfect score: 23

Sequence: 1 DRAK 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	4	14	US-10-199-285-1
2	23	100.0	4	14	US-10-076-071-1
3	23	100.0	4	14	US-10-186-168-1
4	23	100.0	4	14	US-10-205-110-35
5	23	100.0	4	14	US-10-300-664-1
6	23	100.0	5	12	US-10-436-549-374
7	23	100.0	5	12	US-10-436-549-422
8	23	100.0	5	14	US-10-205-110-42
9	23	100.0	6	12	US-09-740-821-3
10	23	100.0	7	14	US-10-205-110-47
11	23	100.0	7	15	US-10-393-992-2
12	23	100.0	8	14	US-10-073-118-41
13	23	100.0	9	14	US-10-205-110-48
14	23	100.0	10	10	US-09-572-404B-2520
15	23	100.0	10	10	US-09-572-404B-2522

16	23	100.0	11	14	US-10-205-110-49	Sequence 49, Appl
17	23	100.0	12	10	US-09-846-347-1	Sequence 1, Appl
18	23	100.0	12	14	US-10-076-071-3	Sequence 3, Appl
19	23	100.0	12	14	US-10-076-071-6	Sequence 6, Appl
20	23	100.0	12	14	US-10-186-168-3	Sequence 3, Appl
21	23	100.0	12	14	US-10-186-168-6	Sequence 6, Appl
22	23	100.0	12	14	US-10-300-664-3	Sequence 3, Appl
23	23	100.0	12	14	US-10-300-664-6	Sequence 6, Appl
24	23	100.0	13	9	US-09-845-764-1	Sequence 1, Appl
25	23	100.0	15	14	US-10-073-118-40	Sequence 40, Appl
26	23	100.0	17	9	US-09-845-727-1	Sequence 1, Appl
27	23	100.0	24	9	US-09-846-328-1	Sequence 1, Appl
28	23	100.0	24	10	US-09-833-041-7	Sequence 7, Appl
29	23	100.0	24	10	US-09-833-117-7	Sequence 7, Appl
30	23	100.0	24	10	US-09-832-501-7	Sequence 7, Appl
31	23	100.0	24	11	US-09-833-118-7	Sequence 7, Appl
32	23	100.0	24	11	US-09-833-245-7	Sequence 7, Appl
33	23	100.0	24	12	US-09-832-929-7	Sequence 7, Appl
34	23	100.0	26	9	US-09-846-329-1	Sequence 1, Appl
35	23	100.0	28	14	US-10-073-118-39	Sequence 39, Appl
36	23	100.0	30	14	US-10-073-118-38	Sequence 38, Appl
37	23	100.0	38	12	US-10-424-599-276943	Sequence 276943, A
38	23	100.0	39	16	US-10-437-963-142640	Sequence 142640, A
39	23	100.0	41	12	US-10-424-599-214427	Sequence 214427, A
40	23	100.0	42	14	US-10-044-967-19	Sequence 19, Appl
41	23	100.0	49	16	US-10-437-963-157961	Sequence 157961, A
42	23	100.0	52	16	US-10-437-963-190243	Sequence 190243, A
43	23	100.0	53	9	US-09-864-761-38159	Sequence 38159, A
44	23	100.0	55	16	US-10-767-701-52864	Sequence 52864, A
45	23	100.0	56	12	US-10-424-599-173176	Sequence 173176, A
46	23	100.0	58	12	US-10-335-977-6310	Sequence 6310, Ap
47	23	100.0	61	12	US-10-424-599-193616	Sequence 193616, A
48	23	100.0	65	12	US-10-424-599-166022	Sequence 166022, A
49	23	100.0	67	12	US-10-424-599-186243	Sequence 186243, A
50	23	100.0	67	12	US-10-424-599-201097	Sequence 201097, A
51	23	100.0	67	12	US-10-424-599-274256	Sequence 274256, A
52	23	100.0	69	12	US-10-424-599-148001	Sequence 148001, A
53	23	100.0	69	12	US-10-424-599-180109	Sequence 180109, A
54	23	100.0	72	11	US-09-864-408A-8000	Sequence 8000, Ap
55	23	100.0	73	11	US-09-864-408A-7866	Sequence 7866, Ap
56	23	100.0	75	12	US-10-424-599-239687	Sequence 239687, A
57	23	100.0	75	12	US-10-424-599-247714	Sequence 247714, A
58	23	100.0	78	16	US-10-437-963-153472	Sequence 153472, A
59	23	100.0	80	12	US-10-424-599-143536	Sequence 143536, A
60	23	100.0	82	12	US-10-424-599-217330	Sequence 217330, A
61	23	100.0	82	12	US-10-424-599-183111	Sequence 183111, A
62	23	100.0	83	16	US-10-437-963-198071	Sequence 198071, A
63	23	100.0	89	12	US-10-424-599-148761	Sequence 148761, A
64	23	100.0	89	12	US-10-424-599-259289	Sequence 259289, A
65	23	100.0	89	16	US-10-437-963-146897	Sequence 146897, A
66	23	100.0	92	15	US-10-264-049-2574	Sequence 2574, Ap
67	23	100.0	95	12	US-10-424-599-247087	Sequence 247087, A
68	23	100.0	96	9	US-09-867-550-390	Sequence 390, App
69	23	100.0	97	12	US-10-424-599-192596	Sequence 192596, A
70	23	100.0	97	12	US-10-424-599-194341	Sequence 194341, A
71	23	100.0	99	16	US-10-437-963-140971	Sequence 140971, A
72	23	100.0	100	16	US-10-437-963-202982	Sequence 202982, A
73	23	100.0	102	16	US-10-424-599-201029	Sequence 201029, A
74	23	100.0	102	16	US-10-437-963-116191	Sequence 116191, A
75	23	100.0	104	12	US-09-764-877-1268	Sequence 1268, Ap
76	23	100.0	104	12	US-10-282-122A-56310	Sequence 56310, A
77	23	100.0	104	15	US-10-282-122A-72146	Sequence 72146, A
78	23	100.0	104	15	US-10-242-515-1268	Sequence 1268, Ap
79	23	100.0	106	12	US-10-424-599-200360	Sequence 200360, A
80	23	100.0	117	9	US-09-764-864-1446	Sequence 1446, Ap
81	23	100.0	117	10	US-09-764-891-3106	Sequence 3106, Ap
82	23	100.0	117	12	US-10-424-599-158248	Sequence 158248, A
83	23	100.0	117	12	US-10-091-414-132	Sequence 132, App
84	23	100.0	117	16	US-10-437-963-180787	Sequence 180787, A
85	23	100.0	118	12	US-10-424-599-284785	Sequence 284785, A
86	23	100.0	119	12	US-10-424-599-192119	Sequence 192119, A
87	23	100.0	120	16	US-10-767-701-55284	Sequence 55284, A
88	23	100.0	121	9	US-09-764-864-1017	Sequence 1017, Ap

89	23	100.0	121	16	US-10-437-963-118103	Sequence 118103,	162	274	9	US-09-836-607-3	Sequence 3, Appli
90	23	100.0	125	16	US-10-767-701-58692	Sequence 58692, A	163	275	10	US-09-421-112-3	Sequence 3, Appli
91	23	100.0	130	12	US-10-424-599-184065	Sequence 184065,	164	276	10	US-10-425-114-46896	Sequence 46896, A
92	23	100.0	134	12	US-10-174-693-316	Sequence 316, App	165	276	10	US-09-811-007-44	Sequence 44, Appl
93	23	100.0	138	16	US-10-437-963-161970	Sequence 161970,	166	276	13	US-10-062-624-44	Sequence 44, Appl
94	23	100.0	145	12	US-10-424-599-272563	Sequence 272563,	167	276	13	US-10-059-964-42	Sequence 42, Appl
95	23	100.0	146	16	US-10-767-701-54038	Sequence 54038, A	168	276	14	US-10-062-051-44	Sequence 44, Appl
96	23	100.0	148	15	US-10-264-049-3303	Sequence 3303, App	168	276	14	US-10-062-920-44	Sequence 44, Appl
97	23	100.0	150	16	US-10-767-701-48747	Sequence 48747, A	170	276	14	US-10-314-639-42	Sequence 42, Appl
98	23	100.0	151	16	US-10-767-701-55741	Sequence 55741, A	171	276	16	US-10-408-765A-199	Sequence 199, App
99	23	100.0	155	9	US-09-738-626-5382	Sequence 5382, App	172	277	9	US-09-826-212-12	Sequence 12, Appl
100	23	100.0	156	16	US-10-437-963-196690	Sequence 196690,	173	277	9	US-09-852-845-2	Sequence 2, Appli
101	23	100.0	158	16	US-10-767-701-34542	Sequence 34542, A	174	277	9	US-09-804-200-2	Sequence 2, Appli
102	23	100.0	163	16	US-10-424-599-253624	Sequence 253624,	175	277	9	US-09-880-939-2	Sequence 2, Appli
103	23	100.0	163	16	US-10-437-963-108254	Sequence 108254,	176	277	9	US-09-768-779A-5	Sequence 5, Appli
104	23	100.0	163	16	US-10-437-963-183760	Sequence 183760,	177	277	9	US-09-935-727-14	Sequence 14, Appl
105	23	100.0	163	16	US-10-767-701-34475	Sequence 34475, A	178	277	14	US-10-140-164-6	Sequence 6, Appli
106	23	100.0	164	12	US-10-112-944-831	Sequence 831, App	179	277	14	US-10-046-433-3	Sequence 3, Appli
107	23	100.0	165	12	US-10-424-599-229903	Sequence 229903,	180	277	14	US-10-291-480-5	Sequence 5, Appli
108	23	100.0	168	14	US-10-219-220-69	Sequence 69, Appl	181	277	14	US-10-186-643-12	Sequence 12, Appl
109	23	100.0	173	12	US-10-282-122A-51039	Sequence 51039, A	182	277	14	US-10-207-655-158	Sequence 158, App
110	23	100.0	174	9	US-09-818-066-41	Sequence 41, Appl	183	277	14	US-10-073-333A-6	Sequence 6, Appli
111	23	100.0	175	12	US-10-282-122A-63331	Sequence 63331, A	184	277	14	US-10-326-929-2	Sequence 2, Appli
112	23	100.0	176	16	US-10-767-701-59057	Sequence 59057, A	185	277	15	US-10-323-274C-2	Sequence 2, Appli
113	23	100.0	175	12	US-10-424-599-245767	Sequence 245767,	186	277	15	US-10-418-242-14	Sequence 14, Appl
114	23	100.0	177	9	US-09-738-626-6375	Sequence 6375, Ap	187	277	16	US-10-646-308-28	Sequence 28, Appl
115	23	100.0	178	12	US-10-282-122A-71251	Sequence 71251, A	188	277	16	US-10-762-489-2	Sequence 2, Appli
116	23	100.0	179	16	US-10-767-701-54995	Sequence 54995, A	189	279	12	US-10-425-114-70568	Sequence 70568, A
117	23	100.0	181	16	US-10-767-701-34323	Sequence 34323, A	190	280	9	US-09-846-808-18	Sequence 18, Appl
118	23	100.0	182	12	US-10-424-599-235243	Sequence 235243,	191	280	10	US-09-811-007-14	Sequence 14, Appl
119	23	100.0	182	12	US-10-425-114-67879	Sequence 67879, A	192	280	13	US-10-062-994-17	Sequence 17, Appl
120	23	100.0	184	12	US-10-282-122A-69208	Sequence 69208, A	193	280	13	US-10-062-624-14	Sequence 14, Appl
121	23	100.0	185	16	US-10-437-963-108948	Sequence 108948,	194	280	13	US-10-059-964-12	Sequence 12, Appl
122	23	100.0	187	12	US-10-424-599-218692	Sequence 218692,	195	280	13	US-10-062-994-17	Sequence 17, Appl
123	23	100.0	187	16	US-10-767-701-34450	Sequence 34450, A	196	280	14	US-10-062-051-14	Sequence 14, Appl
124	23	100.0	195	13	US-10-074-956-24	Sequence 24, Appl	197	280	14	US-10-284-986-18	Sequence 18, Appl
125	23	100.0	201	14	US-10-029-386-33141	Sequence 33141, A	198	280	14	US-10-062-920-14	Sequence 14, Appl
126	23	100.0	201	16	US-10-767-701-62716	Sequence 62716, A	199	280	14	US-10-314-639-12	Sequence 12, Appl
127	23	100.0	204	12	US-10-425-114-40649	Sequence 40649, A	200	280	14	US-10-369-293-18	Sequence 18, Appl
128	23	100.0	208	15	US-10-369-493-17893	Sequence 17893, A	201	280	14	US-10-285-042-18	Sequence 18, Appl
129	23	100.0	208	16	US-10-437-963-169002	Sequence 169002,	202	280	16	US-10-722-077-17	Sequence 17, Appl
130	23	100.0	210	12	US-10-425-114-68348	Sequence 68348, A	203	282	16	US-10-767-701-44132	Sequence 44132, A
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132	23	100.0	218	12	US-10-424-599-202967	Sequence 202967,	205	288	13	US-10-059-964-32	Sequence 32, Appl
133	23	100.0	218	12	US-10-425-114-44794	Sequence 44794, A	206	288	14	US-10-314-639-32	Sequence 32, Appl
134	23	100.0	220	16	US-10-437-963-164459	Sequence 164459,	207	289	12	US-10-282-122A-77758	Sequence 77758, A
135	23	100.0	221	12	US-10-424-599-192720	Sequence 192720,	208	289	12	US-10-012-819-142	Sequence 142, App
136	23	100.0	221	12	US-10-424-599-202354	Sequence 202354,	209	289	16	US-10-408-765A-1532	Sequence 1532, App
137	23	100.0	221	12	US-10-424-599-208873	Sequence 208873,	210	292	12	US-10-282-122A-53986	Sequence 53986, A
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139	23	100.0	222	12	US-10-425-114-40599	Sequence 40599, A	212	292	12	US-10-282-122A-58192	Sequence 58192, A
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141	23	100.0	223	12	US-10-282-122A-63416	Sequence 63416, A	213	295	12	US-10-425-114-64234	Sequence 64234, A
142	23	100.0	224	12	US-10-282-122A-64091	Sequence 64091, A	214	296	12	US-10-282-122A-68541	Sequence 68541, A
143	23	100.0	231	14	US-10-386-972-2	Sequence 2, Appli	215	298	9	US-09-801-368-66	Sequence 66, Appl
144	23	100.0	231	16	US-10-767-605-2	Sequence 2, Appli	216	298	15	US-10-369-493-1475	Sequence 1475, Ap
145	23	100.0	233	12	US-10-425-114-37940	Sequence 37940, A	217	298	16	US-10-369-566-2274	Sequence 2274, Ap
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148	23	100.0	239	12	US-10-012-819-216	Sequence 216, App	220	306	9	US-09-925-297-601	Sequence 601, App
149	23	100.0	240	10	US-09-764-891-2917	Sequence 2917, App	221	309	12	US-10-282-122A-61029	Sequence 61029, A
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152	23	100.0	247	9	US-09-815-242-13269	Sequence 13269, A	224	316	11	US-09-764-875-872	Sequence 872, App
153	23	100.0	250	12	US-10-424-599-202356	Sequence 202356,	225	318	12	US-10-282-122A-63277	Sequence 63277, A
154	23	100.0	252	12	US-10-424-599-268532	Sequence 268532,	226	319	12	US-10-112-944-379	Sequence 379, App
155	23	100.0	256	12	US-10-335-977-6319	Sequence 6319, App	227	319	15	US-10-369-493-10195	Sequence 10195, A
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157	23	100.0	261	12	US-10-424-599-166711	Sequence 166711,	229	326	16	US-10-437-963-187546	Sequence 187546, A
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	23	100.0	273	16	US-10-437-963-177576	Sequence 177576,	234	336	12	US-10-282-122A-77325	Sequence 77325, A

235	23	100.0	336	12	US-10-170-385-369	Sequence 369, App	308	14	US-10-332-795-3	Sequence 3, Appli
236	23	100.0	342	12	US-10-343-650A-104	Sequence 104, App	309	471	US-10-437-963-143190	Sequence 143190,
237	23	100.0	343	12	US-10-282-122A-78434	Sequence 78434, A	310	472	US-10-425-114-63736	Sequence 63736, A
238	23	100.0	345	14	US-10-209-967-15	Sequence 15, Appl	311	472	US-10-421-654-42	Sequence 42, Appl
239	23	100.0	345	14	US-10-209-967-16	Sequence 16, Appl	312	473	US-10-424-599-235245	Sequence 235245,
240	23	100.0	345	16	US-10-767-701-39572	Sequence 39572, A	313	473	US-10-004-378A-104	Sequence 104, App
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243	23	100.0	347	9	US-09-828-302-14	Sequence 14, Appl	316	474	US-10-004-378A-105	Sequence 105, App
244	23	100.0	353	12	US-10-282-122A-70497	Sequence 70497, A	317	474	US-10-004-378A-106	Sequence 106, App
245	23	100.0	357	12	US-10-282-122A-70508	Sequence 70508, A	318	482	US-10-424-599-195294	Sequence 195294,
246	23	100.0	357	12	US-10-282-122A-70512	Sequence 70512, A	319	482	US-10-378-558A-22	Sequence 22, Appl
247	23	100.0	357	12	US-10-282-122A-70521	Sequence 70521, A	320	484	US-09-882-227-518	Sequence 518, App
248	23	100.0	357	12	US-10-282-122A-70567	Sequence 70567, A	321	484	US-10-282-122A-66865	Sequence 66865, A
249	23	100.0	357	12	US-10-282-122A-70593	Sequence 70593, A	322	484	US-10-406-686A-29	Sequence 29, Appl
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252	23	100.0	357	12	US-10-282-122A-71069	Sequence 71069, A	325	485	US-10-369-493-16926	Sequence 16926, A
253	23	100.0	357	12	US-10-282-122A-71104	Sequence 71104, A	326	485	US-10-408-765A-2297	Sequence 2297, Ap
254	23	100.0	357	12	US-10-282-122A-71243	Sequence 71243, A	327	485	US-10-741-601-288	Sequence 288, App
255	23	100.0	360	9	US-09-815-242-11378	Sequence 11378, A	328	485	US-10-741-601-289	Sequence 289, App
256	23	100.0	360	12	US-10-282-122A-58823	Sequence 58823, A	329	486	US-09-312-762A-15	Sequence 15, Appl
257	23	100.0	360	12	US-10-425-114-42197	Sequence 42197, A	330	497	US-10-437-963-130126	Sequence 130126,
258	23	100.0	360	12	US-10-335-977-6956	Sequence 6956, Ap	331	498	US-10-425-114-63735	Sequence 63735, A
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262	23	100.0	375	12	US-10-335-977-6957	Sequence 6957, Ap	335	503	US-10-369-493-4118	Sequence 4118, Ap
263	23	100.0	378	9	US-09-860-670-86	Sequence 86, Appl	336	504	US-10-369-493-12595	Sequence 12595, A
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265	23	100.0	378	11	US-09-955-999-69	Sequence 69, Appl	338	508	US-10-465-217-1	Sequence 1, Appli
266	23	100.0	378	15	US-10-764-875-1153	Sequence 1153, Ap	339	508	US-10-434-588-4	Sequence 4, Appli
267	23	100.0	378	15	US-10-227-646-86	Sequence 86, Appl	340	510	US-10-289-762-639	Sequence 58366, A
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269	23	100.0	382	12	US-10-424-599-246632	Sequence 246632, A	342	518	US-10-389-647-421	Sequence 421, App
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271	23	100.0	389	15	US-10-369-493-23255	Sequence 23255, A	344	523	US-10-437-963-120061	Sequence 120061,
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273	23	100.0	394	12	US-10-627-476-224	Sequence 224, App	346	527	US-10-437-963-113042	Sequence 113042,
274	23	100.0	396	15	US-10-369-493-8066	Sequence 8066, Ap	347	534	US-09-312-762A-4	Sequence 4, Appli
275	23	100.0	397	15	US-10-369-493-261	Sequence 261, App	348	534	US-09-312-762A-5	Sequence 5, Appli
276	23	100.0	400	15	US-10-369-493-21850	Sequence 21850, A	349	534	US-10-755-889-336	Sequence 336, App
277	23	100.0	402	15	US-10-369-493-3740	Sequence 3740, Ap	350	535	US-09-312-762A-10	Sequence 10, Appl
278	23	100.0	403	15	US-10-369-493-19185	Sequence 19185, A	351	535	US-09-312-762A-14	Sequence 14, Appl
279	23	100.0	412	11	US-09-930-512-75	Sequence 75, Appl	352	535	US-10-282-122A-49335	Sequence 49335, A
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281	23	100.0	417	15	US-10-369-493-10765	Sequence 10765, A	354	541	US-10-408-765A-2275	Sequence 2275, Ap
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283	23	100.0	420	15	US-10-369-493-10221	Sequence 10221, A	356	547	US-10-424-599-187086	Sequence 187086,
284	23	100.0	422	15	US-10-289-762-1088	Sequence 1088, Ap	357	552	US-10-425-114-67035	Sequence 67035, A
285	23	100.0	423	15	US-10-023-634-83	Sequence 83, Appl	358	553	US-10-437-963-194394	Sequence 194394,
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287	23	100.0	435	15	US-10-369-493-10634	Sequence 10634, A	360	556	US-10-437-963-154446	Sequence 154446,
288	23	100.0	436	15	US-10-369-493-2369	Sequence 2369, Ap	361	558	US-10-369-493-7749	Sequence 7749, Ap
289	23	100.0	436	15	US-10-369-493-18273	Sequence 18273, A	362	562	US-10-282-122A-50623	Sequence 50623, A
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292	23	100.0	441	15	US-10-369-493-17161	Sequence 17161, A	365	570	US-10-043-487-327	Sequence 327, App
293	23	100.0	444	16	US-10-287-226-370	Sequence 370, App	366	575	US-10-369-493-10343	Sequence 10343, A
294	23	100.0	444	16	US-10-287-226-372	Sequence 372, App	367	585	US-09-929-552-2	Sequence 2, Appli
295	23	100.0	445	12	US-10-282-122A-52444	Sequence 52444, A	368	585	US-09-932-613-445	Sequence 445, App
296	23	100.0	447	15	US-10-104-047-2123	Sequence 2123, Ap	369	585	US-09-984-010-26	Sequence 26, Appl
297	23	100.0	447	16	US-10-437-963-16961	Sequence 16961, A	370	585	US-09-833-041-18	Sequence 18, Appl
298	23	100.0	448	10	US-09-769-970-2	Sequence 2, Appli	371	585	US-09-833-117-18	Sequence 18, Appl
299	23	100.0	449	15	US-10-051-874-68	Sequence 68, Appl	372	585	US-09-932-322-445	Sequence 445, App
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301	23	100.0	453	16	US-10-767-701-40181	Sequence 40181, A	374	585	US-09-833-118-18	Sequence 18, Appl
302	23	100.0	455	16	US-10-437-963-168134	Sequence 168134, A	375	585	US-09-833-245-18	Sequence 18, Appl
303	23	100.0	465	15	US-10-369-493-9941	Sequence 9941, Ap	376	585	US-10-424-999-11	Sequence 11, Appl
304	23	100.0	466	12	US-10-425-114-64356	Sequence 64356, A	377	585	US-10-425-000-31	Sequence 31, Appl
305	23	100.0	467	16	US-10-437-963-151306	Sequence 151306, A	378	585	US-10-433-108-34	Sequence 34, Appl
306	23	100.0	468	16	US-10-437-963-111279	Sequence 111279, A	379	585	US-10-602-141-3	Sequence 3, Appli
307	23	100.0	469	9	US-09-738-626-3908	Sequence 3908, Ap	380	585	US-09-832-929-18	Sequence 18, Appl

381	23	100.0	585	13	US-10-153-064-5	Sequence 5, Appl	454	23	100.0	660	14	US-10-153-604A-90	Sequence 90, Appl
382	23	100.0	585	14	US-10-153-604A-5	Sequence 5, Appl	455	23	100.0	660	14	US-10-153-604A-93	Sequence 93, Appl
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384	23	100.0	585	14	US-10-319-263-2	Sequence 2, Appl	457	23	100.0	668	12	US-10-282-122A-72916	Sequence 102, App
385	23	100.0	585	14	US-10-414-469-1	Sequence 1, Appl	458	23	100.0	668	14	US-10-153-064-102	Sequence 102, App
386	23	100.0	585	14	US-10-414-469-2	Sequence 2, Appl	459	23	100.0	670	16	US-10-408-765A-996	Sequence 996, App
387	23	100.0	585	14	US-10-413-831-1	Sequence 1, Appl	460	23	100.0	671	16	US-10-363-829-452	Sequence 452, App
388	23	100.0	585	14	US-10-413-831-2	Sequence 2, Appl	461	23	100.0	672	12	US-10-424-999-15	Sequence 15, Appl
389	23	100.0	585	15	US-10-413-832-1	Sequence 1, Appl	462	23	100.0	672	12	US-10-425-000-35	Sequence 35, Appl
390	23	100.0	585	15	US-10-413-832-2	Sequence 2, Appl	463	23	100.0	672	15	US-10-233-675A-15	Sequence 15, Appl
391	23	100.0	585	15	US-10-414-386-1	Sequence 1, Appl	464	23	100.0	674	12	US-10-424-999-14	Sequence 14, Appl
392	23	100.0	585	15	US-10-414-386-2	Sequence 2, Appl	465	23	100.0	674	12	US-10-425-000-34	Sequence 34, Appl
393	23	100.0	585	15	US-10-233-675A-11	Sequence 11, Appl	466	23	100.0	674	15	US-10-233-675A-14	Sequence 14, Appl
394	23	100.0	585	15	US-10-462-262-26	Sequence 26, Appl	467	23	100.0	674	16	US-10-437-963-160252	Sequence 160252, A
395	23	100.0	585	16	US-10-361-997-18	Sequence 18, Appl	468	23	100.0	676	13	US-10-153-064-95	Sequence 95, Appl
396	23	100.0	592	12	US-10-042-865-64	Sequence 64, Appl	469	23	100.0	676	13	US-10-153-064-98	Sequence 98, Appl
397	23	100.0	597	14	US-10-017-161-800	Sequence 800, App	470	23	100.0	676	13	US-10-153-064-104	Sequence 104, App
398	23	100.0	604	10	US-09-984-010-7	Sequence 7, Appl	471	23	100.0	676	13	US-10-153-064-127	Sequence 127, App
399	23	100.0	604	16	US-10-408-765A-55	Sequence 55, Appl	472	23	100.0	676	13	US-10-153-064-129	Sequence 129, App
400	23	100.0	609	10	US-09-919-039-370	Sequence 370, App	473	23	100.0	676	14	US-10-153-064A-95	Sequence 95, Appl
401	23	100.0	609	12	US-10-424-999-215539	Sequence 215539, A	474	23	100.0	676	14	US-10-153-064A-98	Sequence 98, Appl
402	23	100.0	609	12	US-10-609-346-12	Sequence 12, Appl	475	23	100.0	676	14	US-10-153-064A-104	Sequence 104, App
403	23	100.0	609	13	US-10-153-064-7	Sequence 7, Appl	476	23	100.0	676	14	US-10-153-064A-127	Sequence 127, App
404	23	100.0	609	14	US-10-153-064A-7	Sequence 7, Appl	477	23	100.0	676	14	US-10-153-064A-129	Sequence 129, App
405	23	100.0	609	14	US-10-365-623-23	Sequence 23, Appl	478	23	100.0	677	13	US-10-153-064-125	Sequence 125, App
406	23	100.0	609	16	US-10-408-765A-2	Sequence 2, Appl	479	23	100.0	677	14	US-10-153-064A-125	Sequence 125, App
407	23	100.0	610	9	US-09-984-186-2	Sequence 2, Appl	480	23	100.0	678	16	US-10-437-963-105320	Sequence 105320, A
408	23	100.0	610	14	US-10-237-667-2	Sequence 2, Appl	481	23	100.0	680	13	US-10-153-064-123	Sequence 123, App
409	23	100.0	610	14	US-10-237-708-2	Sequence 2, Appl	482	23	100.0	680	14	US-10-153-064A-123	Sequence 123, App
410	23	100.0	610	14	US-10-237-866-2	Sequence 2, Appl	483	23	100.0	680	14	US-10-153-064-92	Sequence 92, Appl
411	23	100.0	610	14	US-10-237-871-2	Sequence 2, Appl	484	23	100.0	684	14	US-10-153-064A-92	Sequence 92, Appl
412	23	100.0	610	14	US-10-237-624-2	Sequence 2, Appl	485	23	100.0	687	12	US-10-424-999-17	Sequence 17, Appl
413	23	100.0	610	16	US-10-702-536-2	Sequence 2, Appl	486	23	100.0	687	12	US-10-425-000-37	Sequence 37, Appl
414	23	100.0	610	16	US-10-702-536-2	Sequence 2, Appl	487	23	100.0	687	12	US-10-233-675A-17	Sequence 17, Appl
415	23	100.0	610	16	US-10-767-701-46127	Sequence 46127, A	488	23	100.0	688	12	US-10-424-999-18	Sequence 18, Appl
416	23	100.0	615	12	US-10-282-122A-47612	Sequence 47612, A	489	23	100.0	688	12	US-10-425-000-38	Sequence 38, Appl
417	23	100.0	615	12	US-10-282-122A-49108	Sequence 49108, A	490	23	100.0	688	15	US-10-233-675A-18	Sequence 18, Appl
418	23	100.0	616	12	US-10-433-108-13	Sequence 13, Appl	491	23	100.0	689	12	US-10-424-999-13	Sequence 13, Appl
419	23	100.0	617	16	US-10-361-997-64	Sequence 64, Appl	492	23	100.0	689	12	US-10-425-000-33	Sequence 33, Appl
420	23	100.0	617	16	US-10-361-997-77	Sequence 77, Appl	493	23	100.0	689	15	US-10-233-675A-13	Sequence 13, Appl
421	23	100.0	617	16	US-10-361-997-79	Sequence 79, Appl	494	23	100.0	692	13	US-10-153-064-101	Sequence 101, App
422	23	100.0	624	12	US-10-433-108-16	Sequence 16, Appl	495	23	100.0	692	14	US-10-153-064A-101	Sequence 101, App
423	23	100.0	626	12	US-10-424-999-249044	Sequence 249044, A	496	23	100.0	694	16	US-10-437-963-120426	Sequence 120426, A
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425	23	100.0	631	12	US-10-433-108-14	Sequence 14, Appl	498	23	100.0	701	12	US-10-424-999-283233	Sequence 283233, A
426	23	100.0	631	15	US-10-369-493-4973	Sequence 4973, Ap	499	23	100.0	702	9	US-09-815-242-10117	Sequence 10117, A
427	23	100.0	632	16	US-10-437-963-126138	Sequence 126138, A	500	23	100.0	705	12	US-09-848-909-25	Sequence 25, Appl
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429	23	100.0	639	12	US-10-282-122A-48592	Sequence 48592, A	502	23	100.0	711	12	US-10-282-122A-67509	Sequence 67509, A
430	23	100.0	640	12	US-10-433-108-15	Sequence 15, Appl	503	23	100.0	712	12	US-09-848-909-27	Sequence 27, Appl
431	23	100.0	640	12	US-10-433-108-17	Sequence 17, Appl	504	23	100.0	712	12	US-10-609-346-10	Sequence 10, Appl
432	23	100.0	651	13	US-10-153-064-133	Sequence 133, App	505	23	100.0	714	9	US-09-828-303-21	Sequence 21, Appl
433	23	100.0	651	14	US-10-153-064A-133	Sequence 133, App	506	23	100.0	714	16	US-10-716-089-21	Sequence 21, Appl
434	23	100.0	652	13	US-10-153-064-96	Sequence 96, Appl	507	23	100.0	717	15	US-10-369-493-2178	Sequence 2178, Ap
435	23	100.0	652	13	US-10-153-064-99	Sequence 99, Appl	508	23	100.0	718	12	US-10-609-346-4	Sequence 4, Appl
436	23	100.0	652	13	US-10-153-064-105	Sequence 105, App	509	23	100.0	723	14	US-10-083-357-1343	Sequence 1343, Ap
437	23	100.0	652	13	US-10-153-064-132	Sequence 132, App	510	23	100.0	724	16	US-10-437-963-203858	Sequence 203858, A
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441	23	100.0	652	14	US-10-153-064A-132	Sequence 132, App	514	23	100.0	731	15	US-10-108-260A-2451	Sequence 2451, Ap
442	23	100.0	653	13	US-10-153-064-131	Sequence 131, App	515	23	100.0	734	14	US-10-128-714-3042	Sequence 3042, Ap
443	23	100.0	653	14	US-10-153-064A-131	Sequence 131, App	516	23	100.0	738	14	US-10-270-333-6	Sequence 6, Appl
444	23	100.0	653	16	US-10-437-963-130122	Sequence 130122, A	517	23	100.0	742	12	US-10-424-999-227627	Sequence 227627, A
445	23	100.0	655	16	US-10-361-997-59	Sequence 59, Appl	518	23	100.0	743	16	US-10-149-310-208	Sequence 208, App
446	23	100.0	655	16	US-10-361-997-61	Sequence 61, Appl	519	23	100.0	746	12	US-10-609-346-6	Sequence 6, Appl
447	23	100.0	656	14	US-10-153-064-130	Sequence 130, App	520	23	100.0	749	16	US-10-282-122A-55747	Sequence 55747, A
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529	753	16	US-10-361-997-45	Sequence 45, Appl	602	23	100.0	1855	16	US-10-437-963-144021	Sequence 144021
530	754	12	US-10-424-599-187084	Sequence 187084,	603	23	100.0	1917	16	US-10-408-765A-1313	Sequence 1313, Ap
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534	787	14	US-10-237-667-16	Sequence 16, Appl	607	23	100.0	2215	14	US-10-281-478-4	Sequence 4, Appli
535	787	14	US-10-237-708-16	Sequence 16, Appl	608	23	100.0	2280	16	US-10-437-963-201203	Sequence 201203,
536	787	14	US-10-237-866-16	Sequence 16, Appl	609	23	100.0	2457	12	US-10-282-122A-49854	Sequence 49854, A
537	787	14	US-10-237-871-16	Sequence 16, Appl	610	23	100.0	2671	16	US-10-408-765A-442	Sequence 442, App
538	787	14	US-10-237-824-16	Sequence 16, Appl	611	23	100.0	3079	15	US-10-369-493-2024	Sequence 2024, Ap
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540	787	16	US-10-702-536-16	Sequence 16, Appl	613	23	100.0	3084	14	US-10-262-670-2	Sequence 2, Appli
541	787	16	US-10-702-636-16	Sequence 16, Appl	614	23	100.0	3542	12	US-10-087-013-2	Sequence 2, Appli
542	788	9	US-09-908-193-35	Sequence 35, Appl	615	23	100.0	3692	12	US-10-282-122A-71235	Sequence 71235, A
543	788	14	US-10-073-118-26	Sequence 26, Appl	616	23	100.0	4861	9	US-09-919-497-70	Sequence 70, Appl
544	789	16	US-10-437-963-183376	Sequence 183376,	617	23	100.0	4861	14	US-10-097-534-26	Sequence 26, Appl
545	791	15	US-10-320-800-16	Sequence 16, Appl	618	23	100.0	4861	14	US-10-146-473-49	Sequence 49, Appl
546	796	14	US-10-276-629-16	Sequence 16, Appl	619	23	100.0	4952	15	US-10-051-874-56	Sequence 56, Appl
547	803	16	US-10-389-566-1942	Sequence 1942, Ap	620	23	100.0	5008	15	US-10-051-874-166	Sequence 166, App
548	808	15	US-10-369-493-6771	Sequence 6771, Ap	621	23	100.0	5159	15	US-10-085-198-112	Sequence 112, App
549	810	9	US-09-712-363-281	Sequence 363, Ap	622	23	100.0	5262	15	US-10-051-874-165	Sequence 165, App
550	814	15	US-10-369-493-1953	Sequence 1953, Ap	623	23	100.0	5262	15	US-10-051-874-167	Sequence 167, App
551	824	16	US-10-408-765A-1997	Sequence 1997, Ap	624	23	100.0	5373	16	US-10-408-765A-741	Sequence 741, App
552	834	16	US-10-437-963-115995	Sequence 115995,	625	20	87.0	4	14	US-10-205-110-37	Sequence 37, Appl
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554	865	12	US-10-282-122A-42896	Sequence 42896, A	627	20	87.0	7	12	US-09-768-183-5	Sequence 5, Appli
555	871	12	US-10-282-122A-54240	Sequence 54240, A	628	20	87.0	8	10	US-09-827-542-13	Sequence 13, Appl
556	876	12	US-10-282-122A-77326	Sequence 77326, A	629	20	87.0	9	14	US-10-286-457-301	Sequence 301, App
557	876	12	US-09-848-909-31	Sequence 31, Appl	630	20	87.0	13	12	US-09-764-918-8	Sequence 8, Appli
558	879	12	US-09-848-909-33	Sequence 33, Appl	631	20	87.0	13	12	US-09-768-183-8	Sequence 8, Appli
559	883	16	US-10-472-146-2	Sequence 2, Appli	632	20	87.0	13	15	US-10-436-715-418	Sequence 418, App
560	883	16	US-10-472-146-4	Sequence 4, Appli	633	20	87.0	15	10	US-09-977-797A-136	Sequence 136, App
561	883	16	US-10-472-146-6	Sequence 6, Appli	634	20	87.0	18	14	US-10-174-410-30	Sequence 30, Appl
562	883	16	US-10-472-146-8	Sequence 8, Appli	635	20	87.0	20	14	US-10-174-410-65	Sequence 65, Appl
563	883	16	US-10-472-146-10	Sequence 10, Appl	636	20	87.0	21	14	US-10-029-386-28018	Sequence 28018, A
564	883	16	US-10-472-146-12	Sequence 12, Appl	637	20	87.0	22	14	US-10-247-279-11	Sequence 11, Appl
565	883	16	US-10-472-146-14	Sequence 14, Appl	638	20	87.0	25	9	US-09-864-761-45705	Sequence 45705, A
566	883	16	US-10-472-146-16	Sequence 16, Appl	639	20	87.0	31	9	US-09-864-761-38886	Sequence 38886, A
567	897	15	US-10-369-493-12510	Sequence 12510, A	640	20	87.0	34	10	US-09-933-767-518	Sequence 518, App
568	919	15	US-10-369-493-6768	Sequence 6768, Ap	641	20	87.0	34	12	US-10-424-599-169789	Sequence 169789,
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570	948	12	US-10-021-660-93	Sequence 93, Appl	643	20	87.0	34	14	US-10-023-282-518	Sequence 518, App
571	948	16	US-10-437-963-165672	Sequence 165672,	644	20	87.0	34	16	US-10-437-963-153076	Sequence 153076,
572	949	12	US-10-211-462-30	Sequence 30, Appl	645	20	87.0	39	9	US-09-864-761-46328	Sequence 46328, A
573	949	14	US-10-236-055A-22	Sequence 22, Appl	646	20	87.0	41	16	US-10-437-963-151186	Sequence 151186,
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576	966	16	US-10-437-963-133664	Sequence 133664,	649	20	87.0	45	14	US-10-178-213-72	Sequence 72, Appl
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581	1021	14	US-10-032-585-7387	Sequence 7387, Ap	654	20	87.0	48	10	US-09-933-767-511	Sequence 511, App
582	1043	12	US-10-282-122A-50102	Sequence 50102, A	655	20	87.0	48	12	US-10-004-860-511	Sequence 511, App
583	1097	12	US-10-424-599-189678	Sequence 189678,	656	20	87.0	48	14	US-10-023-282-511	Sequence 511, App
584	1098	15	US-10-161-927-18	Sequence 18, Appl	657	20	87.0	51	9	US-09-867-550-874	Sequence 874, App
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586	1158	15	US-10-369-493-6899	Sequence 6899, Ap	659	20	87.0	52	12	US-10-424-599-201286	Sequence 201286,
587	1166	12	US-10-282-122A-68505	Sequence 68505, A	660	20	87.0	52	12	US-09-864-761-42046	Sequence 42046, A
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589	1184	13	US-10-153-064-89	Sequence 89, Appl	662	20	87.0	53	12	US-10-424-599-277669	Sequence 277669,
590	1184	14	US-10-153-604A-89	Sequence 89, Appl	663	20	87.0	55	16	US-10-437-963-103402	Sequence 103402,
591	1225	15	US-10-158-034-76	Sequence 76, Appl	664	20	87.0	56	12	US-10-282-122A-73442	Sequence 73442, A
592	1230	16	US-10-437-963-133665	Sequence 133665,	665	20	87.0	56	12	US-10-424-599-216359	Sequence 216359,
593	1247	15	US-10-161-493-70	Sequence 70, Appl	666	20	87.0	56	12	US-10-424-599-220552	Sequence 220552,
594	1268	16	US-10-437-963-108730	Sequence 108730,	667	20	87.0	57	14	US-10-211-088-109	Sequence 109, App
595	1314	14	US-10-156-761-13242	Sequence 13242, A	668	20	87.0	58	11	US-09-864-408A-3988	Sequence 3988, Ap
596	1421	16	US-10-437-963-149400	Sequence 149400,	669	20	87.0	58	12	US-10-424-599-255277	Sequence 255277,
597	1465	14	US-10-083-357-1310	Sequence 1310, Ap	670	20	87.0	58	16	US-10-437-963-178197	Sequence 178197,
598	1572	16	US-10-437-963-116757	Sequence 116757,	671	20	87.0	59	12	US-10-424-599-173804	Sequence 173804,
599	1577	14	US-10-017-161-690	Sequence 690, App	672	20	87.0	59	12	US-10-424-599-208528	Sequence 208528,

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686	20	87.0	70	15	US-10-424-599-189223	Sequence 189223,	759	112	12	US-10-424-599-263510	Sequence 161501,
687	20	87.0	71	12	US-10-424-599-219468	Sequence 219468,	760	112	16	US-10-437-963-161501	Sequence 161501,
688	20	87.0	72	14	US-10-315-515-167	Sequence 167, App	761	113	12	US-10-424-599-151134	Sequence 151134,
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691	20	87.0	76	12	US-10-424-599-149255	Sequence 149255,	764	116	14	US-10-078-170-128	Sequence 128, App
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693	20	87.0	77	14	US-10-178-213-74	Sequence 74, Appl	766	116	16	US-10-408-765A-2475	Sequence 2739, Ap
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695	20	87.0	78	12	US-10-424-599-216717	Sequence 216717,	768	116	16	US-10-437-963-176712	Sequence 176712,
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## ALIGNMENTS

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; Publication No. US20030055003A1
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; APPLICANT: DMI BioSciences, Inc.
; APPLICANT: Bar-Or, David
; APPLICANT: Yuki, Richard L.
; TITLE OF INVENTION: USE OF COPPER CHELATORS TO INHIBIT THE INACTIVATION OF PROTEIN C
; FILE REFERENCE: 4172-69
; CURRENT APPLICATION NUMBER: US/10/199,285
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/307,005
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/344,514
; PRIOR FILING DATE: 2001-12-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-199-285-1

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Query Match 100.0%; Score 23; DB 14; Length 4;
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; Sequence 1, Application US/10076071
; Publication No. US20030060408A1
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. Gerald
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagaraja K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor
; FILE REFERENCE: 4172-3-2
; CURRENT APPLICATION NUMBER: US/10/076,071
; CURRENT FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: 09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/283,507
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/816,679
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; PRIOR APPLICATION NUMBER: 60/268,558
; PRIOR FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 9
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US-10-076-071-1

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RESULT 3
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; Publication No. US20030130185A1
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; APPLICANT: Bar-Or, David
; APPLICANT: Curtis, C. G.
; APPLICANT: Lau, Edward
; APPLICANT: Rao, Nagarajo K.R.
; APPLICANT: Winkler, James V.
; APPLICANT: Crook, Wannell M.
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR
; FILE REFERENCE: 4172-3
; CURRENT APPLICATION NUMBER: US/10/186,168
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: US/09/678,202
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,404
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/211,078
; PRIOR FILING DATE: 2000-06-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT

```

; ORGANISM: Homo sapiens  
US-10-186-168-1

Query Match 100.0%; Score 23; DB 14; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
Db 1 DAHK 4

## RESULT 4

US-10-205-110-35  
; Sequence 35, Application US/10205110  
; Publication No. US20030144471A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonassen, Ib  
; APPLICANT: Egel-Mitani, Michi  
; APPLICANT: Balschmidt, per  
; APPLICANT: Markussen, Jan  
; APPLICANT: Diers, Ivan  
; APPLICANT: Kjeldsen, Thomas Borglum  
; TITLE OF INVENTION: Method for Making Acylated Polypeptides  
; FILE REFERENCE: 6289,200-US  
; CURRENT APPLICATION NUMBER: US/10/205,110  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: PA 2001 01141  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/310,793  
; PRIOR FILING DATE: 2001-08-08  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-205-110-35

Query Match 100.0%; Score 23; DB 14; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
Db 1 DAHK 4

## RESULT 5

US-10-300-664-1  
; Sequence 1, Application US/10300664  
; Publication No. US20030158111A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Or, David  
; APPLICANT: Curtis, C. G.  
; APPLICANT: Lau, Edward  
; APPLICANT: Rao, Nagarajo K.R.  
; APPLICANT: Winkler, James V.  
; APPLICANT: Crook, Wannel M.  
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR  
; FILE REFERENCE: 4172-3  
; CURRENT APPLICATION NUMBER: US/10/300,664  
; CURRENT FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: US/09/678,202  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/157,404  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/211,078  
; PRIOR FILING DATE: 2000-06-13  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-300-664-1

Query Match 100.0%; Score 23; DB 14; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
Db 1 DAHK 4

## RESULT 6

US-10-436-549-374  
; Sequence 374, Application US/10436549  
; Publication No. US20040038307A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank D.  
; APPLICANT: Meng, Dr. Xun  
; APPLICANT: Chan, John W.  
; APPLICANT: Zhang, Shengsheng  
; APPLICANT: Benkovic, Stephen J.  
; TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN  
; FILE REFERENCE: ENGB-P01-001  
; CURRENT APPLICATION NUMBER: US/10/436,549  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: 60/379,626  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/393,233  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,235  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,211  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,280  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,197  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,223  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/430,948  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/433,319  
; PRIOR FILING DATE: 2002-12-13  
; PRIOR APPLICATION NUMBER: 60/393,137  
; PRIOR FILING DATE: 2002-07-01  
; NUMBER OF SEQ ID NOS: 614  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 374  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Human  
US-10-436-549-374

Query Match 100.0%; Score 23; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
Db 1 DAHK 4

## RESULT 7

US-10-436-549-422  
; Sequence 422, Application US/10436549  
; Publication No. US20040038307A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank D.

; APPLICANT: Meng, Dr. Xun  
; APPLICANT: Chan, John W.  
; APPLICANT: Zhang, Shengsheng  
; APPLICANT: Benkovic, Stephen J.  
; TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN  
; TITLE OF INVENTION: PROTEIN ANALYSIS  
; FILE REFERENCE: ENGE-P01-001  
; CURRENT APPLICATION NUMBER: US/10/436,549  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: 60/379,626  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/393,233  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,235  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,211  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,280  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,197  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,223  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/430,948  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/433,319  
; PRIOR FILING DATE: 2002-12-13  
; PRIOR APPLICATION NUMBER: 60/393,137  
; PRIOR FILING DATE: 2002-07-01  
; NUMBER OF SEQ ID NOS: 614  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 422  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Human  
US-10-436-549-422

Query Match 100.0%; Score 23; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
Db 2 DAHK 5

RESULT 8  
US-10-205-110-24  
; Sequence 24, Application US/10205110  
; Publication No. US20030144471A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonassen, Ib  
; APPLICANT: Egel-Mitani, Michi  
; APPLICANT: Balschmidt, Per  
; APPLICANT: Markussen, Jan  
; APPLICANT: Diers, Ivan  
; APPLICANT: Kjeldsen, Thomas Borglum  
; TITLE OF INVENTION: Method for Making Acylated Polypeptides  
; FILE REFERENCE: 6289.200-US  
; CURRENT APPLICATION NUMBER: US/10/205,110  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: PA 2001 01141  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/310,793  
; PRIOR FILING DATE: 2001-08-08  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic

US-10-205-110-24  
Query Match 100.0%; Score 23; DB 14; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
Db 2 DAHK 5

RESULT 9  
US-09-740-821-3  
; Sequence 3, Application US/09740821  
; Publication No. US20020006892A1  
; GENERAL INFORMATION:  
; APPLICANT: CARTER, Daniel C.  
; TITLE OF INVENTION: SERUM ALBUMIN COMPOSITIONS FOR USE IN CLEANSING OR DERMATOLOGICAL  
; FILE REFERENCE: P06652US01/BAS  
; CURRENT APPLICATION NUMBER: US/09/740,821  
; CURRENT FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 09/616,962  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-740-821-3

Query Match 100.0%; Score 23; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
Db 1 DAHK 4

RESULT 10  
US-10-205-110-47  
; Sequence 47, Application US/10205110  
; Publication No. US20030144471A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonassen, Ib  
; APPLICANT: Egel-Mitani, Michi  
; APPLICANT: Balschmidt, Per  
; APPLICANT: Markussen, Jan  
; APPLICANT: Diers, Ivan  
; APPLICANT: Kjeldsen, Thomas Borglum  
; TITLE OF INVENTION: Method for Making Acylated Polypeptides  
; FILE REFERENCE: 6289.200-US  
; CURRENT APPLICATION NUMBER: US/10/205,110  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: PA 2001 01141  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/310,793  
; PRIOR FILING DATE: 2001-08-08  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 47  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-205-110-47

Query Match 100.0%; Score 23; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
|  
|  
|  
|  
Db 4 DAHK 7

## RESULT 11

US-10-393-992-2  
; Sequence 2, Application US/10393992  
; Publication No. US2004005645A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanash, David M.  
; APPLICANT: Beer, David G.  
; APPLICANT: Knicker, Rork  
; APPLICANT: Hinderer, Robert  
; TITLE OF INVENTION: PROTEIN MARKERS FOR ESOPHAGEAL CANCER  
; FILE REFERENCE: 108140-00001  
; CURRENT APPLICATION NUMBER: US/10/393,992  
; CURRENT FILING DATE: 2003-03-24  
; PRIOR APPLICATION NUMBER: US/09/508,097  
; PRIOR FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US97/08656  
; PRIOR FILING DATE: 1997-05-29  
; PRIOR APPLICATION NUMBER: 60/018,659  
; PRIOR FILING DATE: 1996-05-30  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Sequence refers to 120, MW 25 kD, pH 5.8, albumin, cld

Query Match 100.0%; Score 23; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
|  
|  
|  
|  
Db 1 DAHK 4

## RESULT 12

US-10-073-118-41  
; Sequence 41, Application US/10073118  
; Publication No. US20030054554A1  
; GENERAL INFORMATION:  
; APPLICANT: BECQUART, JEROME  
; TITLE OF INVENTION: ALBUMIN DERIVATIVES WITH THERAPEUTIC FUNCTIONS  
; FILE REFERENCE: 06832.1429-03  
; CURRENT APPLICATION NUMBER: US/10/073,118  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: 09/551,635  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: 09/004,319  
; PRIOR FILING DATE: 1998-01-08  
; PRIOR APPLICATION NUMBER: 08/479,146  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/295,078  
; PRIOR FILING DATE: 1994-08-26  
; PRIOR APPLICATION NUMBER: 08/121,236  
; PRIOR FILING DATE: 1993-09-13  
; PRIOR APPLICATION NUMBER: 07/955,243  
; PRIOR FILING DATE: 1992-10-01  
; PRIOR APPLICATION NUMBER: 07/561,879  
; PRIOR FILING DATE: 1990-08-02  
; PRIOR APPLICATION NUMBER: FR 89 10480  
; PRIOR FILING DATE: 1989-08-03  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41

; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-073-118-41

Query Match 100.0%; Score 23; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
|  
|  
|  
|  
Db 2 DAHK 5

## RESULT 13

US-10-205-110-48  
; Sequence 48, Application US/10205110  
; Publication No. US20030144471A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonassen, Ib  
; APPLICANT: Egel-Mitani, Michi  
; APPLICANT: Balschmidt, Per  
; APPLICANT: Markussen, Jan  
; APPLICANT: Diers, Ivan  
; APPLICANT: Kjeidsen, Thomas Borglum  
; TITLE OF INVENTION: Method for Making Acylated Polypeptides  
; FILE REFERENCE: 6289.200-US  
; CURRENT APPLICATION NUMBER: US/10/205,110  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: PA 2001 01141  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/310,793  
; PRIOR FILING DATE: 2001-08-08  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-205-110-48

Query Match 100.0%; Score 23; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
|  
|  
|  
|  
Db 6 DAHK 9

## RESULT 14

US-09-572-404B-2520  
; Sequence 2520, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProPatent version 1.0  
; SEQ ID NO 2520  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in SFR55 OR SRP40 OR HRS at 137-146 and may inte

; OTHER INFORMATION: with Sequence 2519 in this patent.  
US-09-572-404B-2520

Query Match 100.0%; Score 23; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 97;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
|||  
Db 4 DAHK 7

RESULT 15

US-09-572-404B-2522  
; Sequence 2522, Application US/09572404B  
; Publication No. US20030078374A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572,404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 2522

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in SFRS5 OR SRP40 OR HRS at 136-145 and may inte  
; OTHER INFORMATION: with Sequence 2521 in this patent.

US-09-572-404B-2522

Query Match

Best Local Similarity 100.0%; Score 23; DB 10; Length 10;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
|||  
Db 5 DAHK 8

Search completed: September 9, 2004, 23:51:05  
Job time : 142 secs